

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:49:50 ; Search time 6173 Seconds
(without alignments)
11028.605 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Match | Query Length | DB | ID | Description |
|------------|-------|---------|--------------|----|----------|-------------------|
| 1 | 958.4 | 68.2 | 5925 | 6 | AR268191 | AR268191 Sequence |
| 2 | 958.4 | 68.2 | 5925 | 6 | AX009712 | AX009712 Sequence |

| | | | | | | | |
|----|-------|------|------|---|----------|----------|------------|
| 3 | 958.4 | 68.2 | 5925 | 6 | AX010972 | AX010972 | Sequence |
| 4 | 937.8 | 66.7 | 2186 | 6 | AX744004 | AX744004 | Sequence |
| 5 | 937.8 | 66.7 | 2790 | 6 | AX744002 | AX744002 | Sequence |
| 6 | 937.8 | 66.7 | 2810 | 6 | AX744006 | AX744006 | Sequence |
| 7 | 936.4 | 66.6 | 1440 | 6 | AX744010 | AX744010 | Sequence |
| 8 | 901.4 | 64.2 | 4691 | 6 | AR370701 | AR370701 | Sequence |
| 9 | 901.4 | 64.2 | 6166 | 6 | AR370702 | AR370702 | Sequence |
| 10 | 779.8 | 55.5 | 6563 | 6 | AR116667 | AR116667 | Sequence |
| 11 | 779.8 | 55.5 | 6563 | 6 | CQ802871 | CQ802871 | Sequence |
| 12 | 779.8 | 55.5 | 6563 | 6 | AR233026 | AR233026 | Sequence |
| 13 | 779.8 | 55.5 | 6563 | 6 | AR237957 | AR237957 | Sequence |
| 14 | 779.8 | 55.5 | 6563 | 6 | BD069220 | BD069220 | Antibody |
| 15 | 751.8 | 53.5 | 2000 | 6 | AX774567 | AX774567 | Sequence |
| 16 | 747.4 | 53.2 | 2178 | 6 | AR048108 | AR048108 | Sequence |
| 17 | 747.4 | 53.2 | 2178 | 6 | AR054190 | AR054190 | Sequence |
| 18 | 747.4 | 53.2 | 2178 | 6 | BD144975 | BD144975 | Method fo |
| 19 | 747.4 | 53.2 | 2178 | 6 | BD145002 | BD145002 | Human gro |
| 20 | 739.6 | 52.6 | 1951 | 6 | AX661181 | AX661181 | Sequence |
| 21 | 739.6 | 52.6 | 6072 | 6 | AX815239 | AX815239 | Sequence |
| 22 | 739.6 | 52.6 | 6072 | 6 | BD069267 | BD069267 | Anti-VEGF |
| 23 | 738.6 | 52.6 | 2143 | 6 | AR123435 | AR123435 | Sequence |
| 24 | 738.6 | 52.6 | 2143 | 6 | BD132751 | BD132751 | Antibody |
| 25 | 738.6 | 52.6 | 2143 | 6 | AR261841 | AR261841 | Sequence |
| 26 | 738.6 | 52.6 | 2143 | 6 | AR491893 | AR491893 | Sequence |
| 27 | 738.6 | 52.6 | 2143 | 6 | BD062169 | BD062169 | Protein r |
| 28 | 738.6 | 52.6 | 6550 | 6 | AR126813 | AR126813 | Sequence |
| 29 | 738.6 | 52.6 | 6550 | 6 | AR162111 | AR162111 | Sequence |
| 30 | 738.6 | 52.6 | 6550 | 6 | BD224164 | BD224164 | Method of |
| 31 | 738.6 | 52.6 | 6550 | 6 | AX832563 | AX832563 | Sequence |
| 32 | 737.4 | 52.5 | 2050 | 6 | CQ861227 | CQ861227 | Sequence |
| 33 | 735.2 | 52.3 | 6072 | 6 | BD010368 | BD010368 | Humanized |
| 34 | 734.6 | 52.3 | 6127 | 6 | AR091716 | AR091716 | Sequence |
| 35 | 734.6 | 52.3 | 6127 | 6 | AR124896 | AR124896 | Sequence |
| 36 | 734.6 | 52.3 | 6127 | 6 | AR169096 | AR169096 | Sequence |
| 37 | 734.6 | 52.3 | 6127 | 6 | BD193235 | BD193235 | Improved |
| 38 | 734.6 | 52.3 | 6127 | 6 | AR454349 | AR454349 | Sequence |
| 39 | 734.6 | 52.3 | 6127 | 6 | AR527679 | AR527679 | Sequence |
| 40 | 689.4 | 49.1 | 2239 | 6 | CQ877236 | CQ877236 | Sequence |
| 41 | 689.4 | 49.1 | 2383 | 6 | CQ877237 | CQ877237 | Sequence |
| 42 | 638.2 | 45.4 | 784 | 9 | AB064058 | AB064058 | Homo sapi |
| 43 | 633.4 | 45.1 | 794 | 9 | AB064136 | AB064136 | Homo sapi |
| 44 | 632.2 | 45.0 | 3169 | 6 | A57359 | A57359 | Sequence 5 |
| 45 | 632.2 | 45.0 | 3169 | 6 | AR096536 | AR096536 | Sequence |

us-10-698-041-1.rng

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:39:44 ; Search time 814 Seconds
(without alignments)
10217.735 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|----------|--------------------|
| 1 | 1405 | 100.0 | 1405 | 13 | ADR16814 | Adr16814 Human bre |
| 2 | 1014.8 | 72.2 | 1522 | 8 | ACC00496 | Acc00496 Humanised |
| 3 | 1003 | 71.4 | 1514 | 12 | ADG64751 | Adg64751 Humanised |
| 4 | 985.8 | 70.2 | 1424 | 13 | ADR16815 | Adr16815 Human bre |
| 5 | 958.4 | 68.2 | 5924 | 3 | AAZ38921 | Aaz38921 hCAT1 bin |
| 6 | 958.4 | 68.2 | 5925 | 3 | AAZ38770 | Aaz38770 hCAT1 c1o |
| 7 | 937.8 | 66.7 | 2186 | 10 | ADD26469 | Add26469 Phagemid |
| 8 | 937.8 | 66.7 | 2790 | 10 | ADD26467 | Add26467 Phagemid |
| 9 | 937.8 | 66.7 | 2810 | 10 | ADD26471 | Add26471 Phagemid |
| 10 | 936.4 | 66.6 | 1440 | 10 | ADD26475 | Add26475 Phagemid |

| | | | | | us-10-698-041-1.rng | |
|----|-------|------|-------|----|---------------------|--------------------|
| 11 | 923 | 65.7 | 1539 | 8 | AAD56202 | Aad56202 X5 antibo |
| 12 | 916.6 | 65.2 | 1539 | 8 | AAD56203 | Aad56203 X5 antibo |
| 13 | 906.2 | 64.5 | 1680 | 12 | ADF83552 | Adf83552 Anti-tete |
| 14 | 901.4 | 64.2 | 4691 | 2 | AAQ92546 | Aaq92546 pComb3 ex |
| 15 | 901.4 | 64.2 | 6166 | 2 | AAQ92547 | Aaq92547 Expressio |
| 16 | 884.8 | 63.0 | 10251 | 10 | ABZ37478 | Abz37478 CJRA05 nu |
| 17 | 856 | 60.9 | 1526 | 12 | ADN97514 | Adn97514 Artificia |
| 18 | 851.8 | 60.6 | 1551 | 12 | ADN97496 | Adn97496 Artificia |
| 19 | 834.8 | 59.4 | 1566 | 12 | ADN97494 | Adn97494 Artificia |
| 20 | 834 | 59.4 | 2154 | 12 | ADN97490 | Adn97490 Artificia |
| 21 | 820.8 | 58.4 | 1572 | 12 | ADN97492 | Adn97492 Artificia |
| 22 | 820 | 58.4 | 2160 | 12 | ADN97488 | Adn97488 Artificia |
| 23 | 796.8 | 56.7 | 5679 | 13 | ADP79576 | Adp79576 Plasmid p |
| 24 | 779.8 | 55.5 | 6563 | 2 | AAV44953 | Aav44953 Anti-IL-8 |
| 25 | 779.8 | 55.5 | 6563 | 2 | AAX90579 | Aax90579 p6G4V11N3 |
| 26 | 779.8 | 55.5 | 6563 | 3 | AAZ87970 | Aaz87970 Nucleotid |
| 27 | 779.8 | 55.5 | 6563 | 3 | AAC65509 | Aac65509 Anti-IL-8 |
| 28 | 779.8 | 55.5 | 6563 | 8 | ABX63890 | Abx63890 Expressio |
| 29 | 779.8 | 55.5 | 6563 | 8 | ABX81417 | Abx81417 Vector p6 |
| 30 | 779.8 | 55.5 | 6563 | 10 | AAD59311 | Aad59311 p6G4V11 N |
| 31 | 767.8 | 54.6 | 6400 | 3 | AAA53389 | Aaa53389 Expressio |
| 32 | 751.8 | 53.5 | 2000 | 9 | ACC70052 | Acc70052 Nucleotid |
| 33 | 747.4 | 53.2 | 2178 | 2 | AAQ25592 | Aaq25592 Encodes 4 |
| 34 | 747.4 | 53.2 | 2178 | 2 | AAV81689 | Aav81689 4D5 Fab m |
| 35 | 739.6 | 52.6 | 6072 | 2 | AAV63493 | Aav63493 Fab-displ |
| 36 | 739.6 | 52.6 | 6072 | 6 | ABN85200 | Abn85200 Phage-dis |
| 37 | 738.6 | 52.6 | 2143 | 2 | AAX03840 | Aax03840 Plasmid p |
| 38 | 738.6 | 52.6 | 2143 | 5 | AAF31463 | Aaf31463 pS 1130 e |
| 39 | 737.4 | 52.5 | 2050 | 13 | ADR47463 | Adr47463 pTTOD(gH3 |
| 40 | 735.2 | 52.3 | 6072 | 2 | AAV71266 | Aav71266 VEGF huma |
| 41 | 734.6 | 52.3 | 6127 | 2 | AAX07474 | Aax07474 Mus muscu |
| 42 | 734.6 | 52.3 | 6127 | 4 | AAF69253 | Aaf69253 Expressio |
| 43 | 734.6 | 52.3 | 6127 | 12 | ADN07022 | Adn07022 F(ab)-pha |
| 44 | 733.2 | 52.2 | 1951 | 6 | ABQ73919 | Abq73919 Plasmid p |
| 45 | 732.8 | 52.2 | 1477 | 12 | ADQ07674 | Adq07674 Nucleotid |

ALIGNMENTS

RESULT 1

ADR16814

ID ADR16814 standard; DNA; 1405 BP.

XX

AC ADR16814;

XX

DT 21-OCT-2004 (first entry)

XX

DE Human breast cancer-specific antibody Fab fragment DNA, Fab14.6.19.

XX

KW Breast cancer; diagnosis; therapy; human; Fab 14.6.19; gene; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

41..700

FT

/*tag= a

FT

/product= "Human breast cancer-specific antibody Fab

FT

fragment Fab14.6.19"

FT

/partial

FT

/note= "No start codon"

FT

CDS

797..1147

FT

/*tag= b

```

us-10-698-041-1.rng
/ product= "Human breast cancer-specific antibody Fab
FT fragment Fab14.6.19"
FT /partial
FT /note= "No start and stop codon"
FT /transl_except= (pos:1145..1147, aa:Ser-Xaa)
XX
PN US2004151724-A1.
XX
PD 05-AUG-2004.
XX
PF 30-OCT-2003; 2003US-00698041.
XX
PR 31-OCT-2002; 2002US-0423052P.
XX
PA (CORO/) CORONELLA-WOOD J.
XX
PI Coronella-wood J;
XX
DR WPI; 2004-570704/55.
DR P-PSDB; ADR16816, ADR16817.
XX
PT New isolated polynucleotides encoding breast cancer-specific antibody Fab
PT fragments 14.6.19 and 14.6.20, useful as clinical reagents for diagnosing
PT or treating breast cancer.
XX
PS Claim 1; SEQ ID NO 1; 36pp; English.
XX
CC The invention provides a breast cancer-specific antibody fragment
CC polynucleotide and its corresponding polypeptide. The invention is useful
CC as clinical reagents for the diagnosis and therapy of breast cancer. The
CC present sequence is human breast cancer-specific antibody Fab fragment
CC DNA, Fab14.6.19.
XX
SQ Sequence 1405 BP; 326 A; 405 C; 381 G; 293 T; 0 U; 0 Other;

Query Match          100.0%; Score 1405; DB 13; Length 1405;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCAGGCCGAGCTCGTGATGACTCAGTC 60
Db      1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCAGGCCGAGCTCGTGATGACTCAGTC 60
Qy     61 TCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120
Db     61 TCCACTCTCCCTGCCCCGTACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120
Qy    121 GAGTCTCCTGCATAGTAATGGATACAAC TATTTGGATTGGTACCTGCAGAAGCCAGGGCA 180
Db    121 GAGTCTCCTGCATAGTAATGGATACAAC TATTTGGATTGGTACCTGCAGAAGCCAGGGCA 180
Qy    181 GTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240
Db    181 GTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240
Qy    241 CAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300
Db    241 CAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300
Qy    301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360
Db    301 TGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360

```

us-10-698-041-1.rng

Qy 361 ACGACTGGAGATTAACGAAGTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA 420
 |||
 Db 361 ACGACTGGAGATTAACGAAGTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA 420

Qy 421 TGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAG 480
 |||
 Db 421 TGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCAG 480

Qy 481 AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG 540
 |||
 Db 481 AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG 540

Qy 541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG 600
 |||
 Db 541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG 600

Qy 601 CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG 660
 |||
 Db 601 CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG 660

Qy 661 CTTGCCCCTCACAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGA 720
 |||
 Db 661 CTTGCCCCTCACAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGA 720

Qy 721 GGAATTTAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780
 |||
 Db 721 GGAATTTAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780

Qy 781 CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCTGG 840
 |||
 Db 781 CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCTGG 840

Qy 841 GGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCA 900
 |||
 Db 841 GGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCA 900

Qy 901 CTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGG 960
 |||
 Db 901 CTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGG 960

Qy 961 GAGTATCACAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGC 1020
 |||
 Db 961 GAGTATCACAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGC 1020

Qy 1021 CAAGAACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTA 1080
 |||
 Db 1021 CAAGAACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTA 1080

Qy 1081 CTGTACACGAGATATTGGGGTCTGTATGCTCACTGGGGCCAGGGAACCCTGGTCACCGT 1140
 |||
 Db 1081 CTGTACACGAGATATTGGGGTCTGTATGCTCACTGGGGCCAGGGAACCCTGGTCACCGT 1140

Qy 1141 CTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCAC 1200
 |||
 Db 1141 CTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCAC 1200

Qy 1201 CTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC 1260
 |||
 Db 1201 CTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC 1260

Qy 1261 GGTGTCGTGGAAGTCAAGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACA 1320
 |||
 Db 1261 GGTGTCGTGGAAGTCAAGCGCCCTGACCAGCGGCGTGCACACCTTCCCGGCTGTCCTACA 1320

us-10-698-041-1.rng

| | | | |
|----|------|--------------------------------------------------------------|------|
| Qy | 1321 | GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC | 1380 |
| | | | |
| Db | 1321 | GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC | 1380 |
| Qy | 1381 | CCAGACCTACATCTGCAACGTGAAT | 1405 |
| | | | |
| Db | 1381 | CCAGACCTACATCTGCAACGTGAAT | 1405 |

us-10-698-041-1.rnpb

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 10:58:17 ; Search time 877 Seconds
(without alignments)
9719.189 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5622541 seqs, 3033355566 residues

Total number of hits satisfying chosen parameters: 11245082

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|-----------------|-------------------|
| 1 | 1405 | 100.0 | 1405 | 18 | US-10-698-041-1 | Sequence 1, Appli |

| | | | | us-10-698-041-1.rnpb | | |
|------|-------|------|-------|----------------------|---------------------|-------------------|
| 2 | 1003 | 71.4 | 1514 | 17 | US-10-251-215-38 | Sequence 38, Appl |
| 3 | 985.8 | 70.2 | 1424 | 18 | US-10-698-041-2 | Sequence 2, Appli |
| 4 | 958.4 | 68.2 | 5925 | 16 | US-10-235-175-78 | Sequence 78, Appl |
| 5 | 923 | 65.7 | 1539 | 18 | US-10-492-729-4 | Sequence 4, Appli |
| 6 | 916.6 | 65.2 | 1539 | 18 | US-10-492-729-12 | Sequence 12, Appl |
| 7 | 884.8 | 63.0 | 10251 | 17 | US-10-045-674-582 | Sequence 582, App |
| 8 | 856 | 60.9 | 1526 | 18 | US-10-679-620-87 | Sequence 87, Appl |
| 9 | 851.8 | 60.6 | 1551 | 18 | US-10-679-620-69 | Sequence 69, Appl |
| 10 | 834.8 | 59.4 | 1566 | 18 | US-10-679-620-67 | Sequence 67, Appl |
| 11 | 834 | 59.4 | 2154 | 18 | US-10-679-620-63 | Sequence 63, Appl |
| 12 | 820.8 | 58.4 | 1572 | 18 | US-10-679-620-65 | Sequence 65, Appl |
| 13 | 820 | 58.4 | 2160 | 18 | US-10-679-620-61 | Sequence 61, Appl |
| 14 | 779.8 | 55.5 | 6563 | 10 | US-09-726-258-61 | Sequence 61, Appl |
| 15 | 739.6 | 52.6 | 1951 | 13 | US-10-011-125-1 | Sequence 1, Appli |
| 16 | 739.6 | 52.6 | 6072 | 9 | US-09-056-160B-99 | Sequence 99, Appl |
| 17 | 739.6 | 52.6 | 6072 | 16 | US-10-234-671-99 | Sequence 99, Appl |
| 18 | 738.6 | 52.6 | 2143 | 9 | US-09-940-166A-5 | Sequence 5, Appli |
| 19 | 738.6 | 52.6 | 2143 | 18 | US-10-762-967-5 | Sequence 5, Appli |
| 20 | 734.6 | 52.3 | 6127 | 9 | US-09-920-171-1 | Sequence 1, Appli |
| 21 | 734.6 | 52.3 | 6127 | 15 | US-10-113-996-1 | Sequence 1, Appli |
| 22 | 734.6 | 52.3 | 6127 | 18 | US-10-791-619-1 | Sequence 1, Appli |
| 23 | 732.8 | 52.2 | 1477 | 19 | US-10-728-420B-116 | Sequence 116, App |
| c 24 | 732.8 | 52.2 | 1477 | 19 | US-10-728-420B-117 | Sequence 117, App |
| 25 | 681.6 | 48.5 | 1730 | 14 | US-10-194-975-108 | Sequence 108, App |
| 26 | 628 | 44.7 | 720 | 17 | US-10-292-088-15 | Sequence 15, Appl |
| 27 | 627.8 | 44.7 | 720 | 17 | US-10-292-088-63 | Sequence 63, Appl |
| 28 | 624.8 | 44.5 | 720 | 17 | US-10-292-088-7 | Sequence 7, Appli |
| 29 | 624.8 | 44.5 | 720 | 17 | US-10-292-088-101 | Sequence 101, App |
| 30 | 624.4 | 44.4 | 720 | 17 | US-10-292-088-55 | Sequence 55, Appl |
| 31 | 623.2 | 44.4 | 720 | 17 | US-10-292-088-79 | Sequence 79, Appl |
| 32 | 621.6 | 44.2 | 720 | 17 | US-10-292-088-39 | Sequence 39, Appl |
| 33 | 620 | 44.1 | 720 | 17 | US-10-292-088-31 | Sequence 31, Appl |
| 34 | 618.8 | 44.0 | 4793 | 18 | US-10-737-290-141 | Sequence 141, App |
| 35 | 612.6 | 43.6 | 1081 | 17 | US-10-466-164-33 | Sequence 33, Appl |
| 36 | 612.2 | 43.6 | 657 | 10 | US-09-972-656-103 | Sequence 103, App |
| 37 | 609.8 | 43.4 | 649 | 19 | US-10-714-079C-8 | Sequence 8, Appli |
| 38 | 606.2 | 43.1 | 944 | 17 | US-10-108-260A-1585 | Sequence 1585, Ap |
| 39 | 604.6 | 43.0 | 968 | 10 | US-09-992-600A-7 | Sequence 7, Appli |
| 40 | 604.6 | 43.0 | 968 | 10 | US-09-924-340-7 | Sequence 7, Appli |
| 41 | 604.6 | 43.0 | 968 | 10 | US-09-992-095B-7 | Sequence 7, Appli |
| 42 | 604.6 | 43.0 | 968 | 10 | US-09-999-570-7 | Sequence 7, Appli |
| 43 | 604.6 | 43.0 | 968 | 14 | US-10-000-489-7 | Sequence 7, Appli |
| 44 | 604.6 | 43.0 | 968 | 14 | US-10-000-986-7 | Sequence 7, Appli |
| 45 | 604.6 | 43.0 | 968 | 16 | US-10-154-678-7 | Sequence 7, Appli |

ALIGNMENTS

RESULT 1

US-10-698-041-1

; Sequence 1, Application US/10698041

; Publication No. US20040151724A1

; GENERAL INFORMATION:

; APPLICANT: Coronella-wood, Julia

; TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer

; FILE REFERENCE: 5051.057

; CURRENT APPLICATION NUMBER: US/10/698,041

; CURRENT FILING DATE: 2003-10-30

; PRIOR APPLICATION NUMBER: US 60/423,052

; PRIOR FILING DATE: 2002-10-31

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: PatentIn version 3.2

us-10-698-041-1.rnpb

; SEQ ID NO 1
; LENGTH: 1405
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-698-041-1

Query Match 100.0%; Score 1405; DB 18; Length 1405;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1405; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCAGGCGGCCGAGCTCGTGATGACTCAGTC 60
      |||
DB      1 AAAATGCCTGGCTGGTTTCGCTACCGTGGCCAGGCGGCCGAGCTCGTGATGACTCAGTC 60

QY     61 TCCACTCTCCCTGCCCCTGACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120
      |||
DB     61 TCCACTCTCCCTGCCCCTGACCCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCA 120

QY    121 GAGTCTCCTGCATAGTAATGGATACAACCTATTTGGATTGGTACCTGCAGAAGCCAGGGCA 180
      |||
DB    121 GAGTCTCCTGCATAGTAATGGATACAACCTATTTGGATTGGTACCTGCAGAAGCCAGGGCA 180

QY    181 GTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240
      |||
DB    181 GTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTT 240

QY    241 CAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300
      |||
DB    241 CAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGA 300

QY    301 TGTTGGGGTTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360
      |||
DB    301 TGTTGGGGTTTTATTACTGCATGCAAGGTCTACAAACTCCTAGGACCTTCGGCCAAGGGAC 360

QY    361 ACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA 420
      |||
DB    361 ACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGA 420

QY    421 TGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG 480
      |||
DB    421 TGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG 480

QY    481 AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG 540
      |||
DB    481 AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAG 540

QY    541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG 600
      |||
DB    541 TGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAG 600

QY    601 CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG 660
      |||
DB    601 CAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAG 660

QY    661 CTTGCCCCTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGA 720
      |||
DB    661 CTTGCCCCTCACAAAGAGCTTCAACAGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGA 720

QY    721 GGAATTTAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780
      |||
DB    721 GGAATTTAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGC 780

QY    781 CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTACGCTGG 840
```

us-10-698-041-1.rnpb

| | | | | |
|----|------|--|---------------------------------------------------------------|------|
| Db | 781 | | CCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTCAGCCTGG | 840 |
| Qy | 841 | | GGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCA | 900 |
| Db | 841 | | GGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCA | 900 |
| Qy | 901 | | CTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGG | 960 |
| Db | 901 | | CTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGG | 960 |
| Qy | 961 | | GAGTATCACAAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGC | 1020 |
| Db | 961 | | GAGTATCACAAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGC | 1020 |
| Qy | 1021 | | CAAGAACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTA | 1080 |
| Db | 1021 | | CAAGAACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTA | 1080 |
| Qy | 1081 | | CTGTACACGAGATATTGGGGGTCGTGATGCTCACTGGGGCCAGGGAACCCTGGTCACCGT | 1140 |
| Db | 1081 | | CTGTACACGAGATATTGGGGGTCGTGATGCTCACTGGGGCCAGGGAACCCTGGTCACCGT | 1140 |
| Qy | 1141 | | CTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCAC | 1200 |
| Db | 1141 | | CTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCCTCCAAGAGCAC | 1200 |
| Qy | 1201 | | CTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC | 1260 |
| Db | 1201 | | CTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGAC | 1260 |
| Qy | 1261 | | GGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCCTACA | 1320 |
| Db | 1261 | | GGTGTCTGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCCTACA | 1320 |
| Qy | 1321 | | GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC | 1380 |
| Db | 1321 | | GTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCAC | 1380 |
| Qy | 1381 | | CCAGACCTACATCTGCAACGTGAAT | 1405 |
| Db | 1381 | | CCAGACCTACATCTGCAACGTGAAT | 1405 |

RESULT 2

US-10-251-215-38

; Sequence 38, Application US/10251215

; Publication No. US20030219839A1

; GENERAL INFORMATION:

; APPLICANT: Bowdish, Katherine S.

; APPLICANT: Kretz-Rommel, Anke

; APPLICANT: Frederickson, Shana

; TITLE OF INVENTION: ANTI-PDGF ANTIBODIES AND METHODS FOR PRODUCING ENGINEERED

; TITLE OF INVENTION: ANTIBODIES

; FILE REFERENCE: 1087-36

; CURRENT APPLICATION NUMBER: US/10/251,215

; CURRENT FILING DATE: 2002-09-20

; PRIOR APPLICATION NUMBER: US 60/323,537

; PRIOR FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: US 60/323,544

; PRIOR FILING DATE: 2001-09-20

; PRIOR APPLICATION NUMBER: US 60/379,980

; PRIOR FILING DATE: 2002-05-13

us-10-698-041-1.rnpb

; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 1514
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Assembled Degenerate Oligonucleotides
US-10-251-215-38

Query Match 71.4%; Score 1003; DB 17; Length 1514;
Best Local Similarity 83.7%; Pred. No. 7e-281;
Matches 1163; Conservative 25; Mismatches 165; Indels 36; Gaps 4;

```
Qy      35 GCGGCCGAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCG 94
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      15 GGGCCCGAGATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGA 74

Qy      95 GCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACTATTTG 154
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      75 GTCACCATCACTTGCCRGGCSAGTCAGRGCATTAGT-----ARYTACTTA 119

Qy     155 GATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAAT 214
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     120 GCCTGGTATCAGCAGAAACCAGGGAAASYTCCTAAGCTCCTGATCTATGATGCATCCGAT 179

Qy     215 CGGGCCTCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTATACACTG 274
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     180 CTGGCATCTGGGGTCCCATCTCGGTTTCARTGGCAGTGGATCTGGGACAGATTWCACTCTC 239

Qy     275 AAAATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAG----- 326
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     240 ACCATCAGCAGCCTGCAGYSTGAAGATGYTGCAACTTATTACTGTCAACAGGGTTATAGT 299

Qy     327 -GTCTACAAACTCCTAGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTG 385
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     300 AGTAGTAATGTTGATAATACTTTCGGCGGAGGGACCGAGGTGGTTCGTCAAACGAACTGTG 359

Qy     386 GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCC 445
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     360 GCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCC 419

Qy     446 TCTGTTGTGTGCCTGCTGAATAAATTCTATCCCAGAGAGGGCCAAAGTACAGTGGAAGGTG 505
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     420 TCTGTTGTGTGCCTGCTGAATAAATTCTATCCCAGAGAGGGCCAAAGTACAGTGGAAGGTG 479

Qy     506 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC 565
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     480 GATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGAC 539

Qy     566 AGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAA 625
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     540 AGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAA 599

Qy     626 GTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAAC 685
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     600 GTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAAC 659

Qy     686 AGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGAATTTAAAATGAAATACCTATTG 745
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     660 AGGGGAGAGTGTTAGTTCTAGATAATTAATTAGGAGGAATTTAAAATGAAATACCTATTG 719

Qy     746 CCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCCAGGTGCAG 805
```

us-10-698-041-1.rnpb

```

db      720 CCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCGAGGTGCAG 779
Qy      806 CTGCAGGAGTCCGGGGGAGGCTTAGTTAGCCTGGGGGGTCCCTGAGACTCTCCTGTGAA 865
db      780 CTGGTGGAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGTCCCTGAGACTCTCCTGTGCA 839
Qy      866 GCCTCTGGATACACCTTCAGCAATTACTGGATGCACTGGGTCCGCCAACCTCCAGGGAAG 925
db      840 GCCTCTGGATTWCYCCYAGTARMWATRKMATRARYTGGGTCCGCCAGGCTCCAGGGAAG 899
Qy      926 GGGCTGGTGTGGGTCTCACGTATTAATGAAGATGGGAGTATCACAAACGACGCGGACTCC 985
db      900 GGGCTGGAGTGGRTCKSATTCATTAAT---ACTGGTAGTAGCGCATACTACGCGAGCTGG 956
Qy      986 GTGAAGGGCCGATCCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGGAAATG 1045
db      957 GCGGAAAGCCGATYCACCATCTCCAGAGACAMCGCCAAGAACTCASTGTATCTGCAAATG 1016
Qy      1046 AACAGTCTGAGAGCCGAGGACACGGCTGTCTATTACTGTACACGAGATATTGGGGGTCTG 1105
db      1017 AACAGCCTGAGAGCCGAGGACACGGCTGTGTATTWCTGTGCGAGAGGTAGTCCTGGTTAC 1076
Qy      1106 GATGCT-----CACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 1156
db      1077 AGTGATGGACTTAACATCTGGGGCCAGGGCACCTGGTCACCGTCTCCTCAGCCTCCACC 1136
Qy      1157 AAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCG 1216
db      1137 AAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAGAGCACCTCTGGGGGCACAGCG 1196
Qy      1217 GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCA 1276
db      1197 GCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCTGTGGAAGTCA 1256
Qy      1277 GGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC 1336
db      1257 GGCGCCCTGACCAGCGGCGTGACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTAC 1316
Qy      1337 TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 1396
db      1317 TCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGC 1376
Qy      1397 AACGTGAAT 1405
db      1377 AACGTGAAT 1385

```

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 07:45:31 ; Search time 4941 Seconds
 (without alignments)
 10823.780 Million cell updates/sec

Title: US-10-698-041-1
 Perfect score: 1405
 Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*
 1: gb_est1:*
 2: gb_est2:*
 3: gb_htc:*
 4: gb_est3:*
 5: gb_est4:*
 6: gb_est5:*
 7: gb_est6:*
 8: gb_gss1:*
 9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query | | DB | ID | Description |
|------------|-------|---------|--------|----|----------|--------------------|
| | | Match | Length | | | |
| 1 | 615.4 | 43.8 | 995 | 5 | BQ712430 | BQ712430 AGENCOURT |
| 2 | 608 | 43.3 | 859 | 4 | BG758795 | BG758795 602713155 |
| 3 | 603.8 | 43.0 | 785 | 6 | CB958366 | CB958366 AGENCOURT |
| 4 | 600.4 | 42.7 | 796 | 6 | CB956719 | CB956719 AGENCOURT |
| 5 | 597.8 | 42.5 | 734 | 6 | CB957433 | CB957433 AGENCOURT |
| 6 | 596.6 | 42.5 | 908 | 4 | BG685179 | BG685179 602637065 |
| 7 | 589.2 | 41.9 | 731 | 6 | CB985070 | CB985070 AGENCOURT |
| 8 | 588.4 | 41.9 | 730 | 4 | BI837183 | BI837183 603089959 |

| | | | | | | | |
|------|-------|------|-----|---|----------|----------|-----------|
| 9 | 587.4 | 41.8 | 958 | 5 | BQ709417 | BQ709417 | AGENCOURT |
| 10 | 585.8 | 41.7 | 880 | 4 | BG755003 | BG755003 | 602711509 |
| 11 | 582.2 | 41.4 | 771 | 6 | CB956254 | CB956254 | AGENCOURT |
| 12 | 576.2 | 41.0 | 753 | 4 | BG756401 | BG756401 | 602715727 |
| 13 | 574.8 | 40.9 | 765 | 6 | CB957191 | CB957191 | AGENCOURT |
| 14 | 574 | 40.9 | 952 | 4 | BG758592 | BG758592 | 602712820 |
| 15 | 572 | 40.7 | 734 | 6 | CB986286 | CB986286 | AGENCOURT |
| 16 | 569.8 | 40.6 | 912 | 4 | BF974515 | BF974515 | 602243421 |
| 17 | 569.4 | 40.5 | 880 | 4 | BG757588 | BG757588 | 602714763 |
| 18 | 565.4 | 40.2 | 766 | 6 | CB956983 | CB956983 | AGENCOURT |
| 19 | 564.2 | 40.2 | 710 | 4 | BI908471 | BI908471 | 603069231 |
| 20 | 563.8 | 40.1 | 774 | 4 | BM007808 | BM007808 | 603617276 |
| 21 | 562.2 | 40.0 | 875 | 4 | BI518518 | BI518518 | 603061638 |
| 22 | 560.2 | 39.9 | 898 | 5 | BQ708918 | BQ708918 | AGENCOURT |
| 23 | 558.2 | 39.7 | 816 | 4 | BI759427 | BI759427 | 603043095 |
| 24 | 556 | 39.6 | 931 | 4 | BG757255 | BG757255 | 602715238 |
| 25 | 556 | 39.6 | 962 | 4 | BI819546 | BI819546 | 603036758 |
| 26 | 552.6 | 39.3 | 934 | 4 | BF974268 | BF974268 | 602243920 |
| 27 | 552.4 | 39.3 | 817 | 6 | CB957285 | CB957285 | AGENCOURT |
| 28 | 550 | 39.1 | 770 | 4 | BG530186 | BG530186 | 602558684 |
| 29 | 548.8 | 39.1 | 839 | 6 | CB986712 | CB986712 | AGENCOURT |
| 30 | 547.4 | 39.0 | 751 | 6 | CB956880 | CB956880 | AGENCOURT |
| 31 | 543.8 | 38.7 | 811 | 4 | BI818338 | BI818338 | 603032958 |
| 32 | 543 | 38.6 | 743 | 6 | CB987308 | CB987308 | AGENCOURT |
| 33 | 542.2 | 38.6 | 824 | 4 | BI824708 | BI824708 | 603033871 |
| 34 | 539.2 | 38.4 | 918 | 4 | BG681688 | BG681688 | 602627806 |
| c 35 | 537.2 | 38.2 | 615 | 2 | AW603541 | AW603541 | RC0-CN002 |
| 36 | 536.4 | 38.2 | 795 | 6 | CB958667 | CB958667 | AGENCOURT |
| 37 | 535.8 | 38.1 | 849 | 7 | CO578998 | CO578998 | ILLUMIGEN |
| 38 | 533 | 37.9 | 706 | 6 | CB956177 | CB956177 | AGENCOURT |
| 39 | 533 | 37.9 | 740 | 6 | CB958744 | CB958744 | AGENCOURT |
| 40 | 532.4 | 37.9 | 726 | 4 | BM007723 | BM007723 | 603617168 |
| 41 | 532.4 | 37.9 | 731 | 6 | CB955606 | CB955606 | AGENCOURT |
| 42 | 531.4 | 37.8 | 697 | 6 | CD684481 | CD684481 | EST1001 h |
| 43 | 531 | 37.8 | 971 | 7 | CO580847 | CO580847 | ILLUMIGEN |
| 44 | 530 | 37.7 | 907 | 5 | BQ708655 | BQ708655 | AGENCOURT |
| 45 | 529.4 | 37.7 | 700 | 4 | BG547577 | BG547577 | 602575404 |

ALIGNMENTS

RESULT 1

BQ712430

LOCUS BQ712430 995 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8352203 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6277729
5', mRNA sequence.

ACCESSION BQ712430

VERSION BQ712430.1 GI:21851329

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 995)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2464 row: j column: 02
High quality sequence stop: 645.

FEATURES Location/Qualifiers
source 1. .995
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6277729"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match 43.8%; Score 615.4; DB 5; Length 995;
Best Local Similarity 96.7%; Pred. No. 2.2e-160;
Matches 639; Conservative 0; Mismatches 21; Indels 1; Gaps 1;

```

Qy      41 GAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 100
      || | |||||||||||||||||||||||||||||||||||||||||||||||||||
Db      67 GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 126

Qy     101 ATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACATATTTGGATTGG 160
      ||||||||||||||||||| ||||||||||||||||||| |||||||
Db     127 ATCTCCTGCAGGTCTAGTCAGAGCCTCCTGCATAGTAATGGATACAACATATTTAGATTGG 186

Qy     161 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCC 220
      ||||||||||||||||||| ||||||||||||||||||| |||||||
Db     187 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTCTAATCGGGCC 246

Qy     221 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTATACACTGAAAATC 280
      ||||||||||||||||||| ||||||||||||||||||| |||||||
Db     247 TCCGGGGTCCCTGACAGGTTTCAGTGGCAGTGGATCAGGCACAGATTTTACACTGAAAATC 306

Qy     281 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTCTACAAACTCCT 340
      ||||||||||||||||||| ||||||||||||||||||| |||||
Db     307 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGCTCTACAAACTCCG 366

Qy     341 AGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAAGTGTGGCTGCACCATCTGTC 400
      || || ||||| ||||| ||||||| |||||||||||||||||||
Db     367 TACACTTTTGGCCAGGGGACCAAGCTGGAGATCAAACGAAGTGTGGCTGCACCATCTGTC 426

```


| | | | |
|----|-----|---------------------------------------------------------------|-----|
| Qy | 401 | TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTG | 460 |
| | | | |
| Db | 427 | TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTG | 486 |
| Qy | 461 | CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA | 520 |
| | | | |
| Db | 487 | CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAA | 546 |
| Qy | 521 | TCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC | 580 |
| | | | |
| Db | 547 | TCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC | 606 |
| Qy | 581 | AGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA | 640 |
| | | | |
| Db | 607 | AGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA | 666 |
| Qy | 641 | GTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTC-AACAGGGGAGAGTGTTA | 699 |
| | | | |
| Db | 667 | GTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCNAACAGGGGAGAGTGTTA | 726 |
| Qy | 700 | G | 700 |
| | | | |
| Db | 727 | G | 727 |

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 12:20:41 ; Search time 121 Seconds
(without alignments)
8981.791 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155500_6534/app_query.fasta_1.15
43

-DB=A_Geneseq_16Dec04 -QFMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10698041 @CGN_1_1_149 @runat_14042005_155500_6534 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | % | | Query | | DB | ID | Description |
|---------------|--------|-------|--------|---|----------|----------|-------------|
| | Score | Match | Length | | | | |
| 1 | 1802 | 72.3 | 628 | 6 | ABJ38670 | Abj38670 | Fab expre |
| 2 | 1802 | 72.3 | 638 | 6 | ADA89103 | Ada89103 | Phage dis |
| 3 | 1802 | 72.3 | 638 | 6 | ADA90139 | Ada90139 | Anti-Abet |
| 4 | 1802 | 72.3 | 638 | 6 | ADA91410 | Ada91410 | Anti-Abet |
| 5 | 1802 | 72.3 | 747 | 7 | ADG74355 | Adg74355 | MSPRO lig |
| 6 | 1768.5 | 70.9 | 490 | 3 | AAY56637 | Aay56637 | hCAT1 bin |
| 7 | 1733 | 69.5 | 484 | 6 | ABR55341 | Abr55341 | Amino aci |
| 8 | 1676 | 67.2 | 537 | 3 | AAB03664 | Aab03664 | Anti-CD18 |
| 9 | 1675 | 67.2 | 698 | 2 | AAW83493 | Aaw83493 | 4D5 Fab m |
| 10 | 1668.5 | 66.9 | 650 | 5 | ABP61241 | Abp61241 | Phage-dis |
| 11 | 1665.5 | 66.8 | 502 | 8 | ADN97515 | Adn97515 | Artificia |
| 12 | 1664.5 | 66.7 | 512 | 8 | ADN97497 | Adn97497 | Artificia |
| 13 | 1660 | 66.6 | 517 | 8 | ADN97495 | Adn97495 | Artificia |
| 14 | 1658 | 66.5 | 519 | 8 | ADN97493 | Adn97493 | Artificia |
| 15 | 1650 | 66.2 | 713 | 8 | ADN97491 | Adn97491 | Artificia |
| 16 | 1648 | 66.1 | 715 | 8 | ADN97489 | Adn97489 | Artificia |
| 17 | 1606.5 | 64.4 | 487 | 6 | ABO27163 | Abo27163 | Humanised |
| 18 | 1282.5 | 51.4 | 712 | 8 | ADN97543 | Adn97543 | Artificia |
| 19 | 1213.5 | 48.7 | 1031 | 5 | ADI46109 | Adi46109 | Single st |
| 20 | 1178 | 47.2 | 483 | 8 | ADN97549 | Adn97549 | Artificia |
| 21 | 1178 | 47.2 | 510 | 8 | ADN97519 | Adn97519 | Artificia |
| 22 | 1178 | 47.2 | 510 | 8 | ADN97501 | Adn97501 | Artificia |
| 23 | 1178 | 47.2 | 700 | 8 | ADN97521 | Adn97521 | Artificia |
| 24 | 1142 | 45.8 | 219 | 8 | ADR16817 | Adr16817 | Human bre |
| 25 | 1115.5 | 44.7 | 500 | 7 | ADD13792 | Add13792 | Plasmid p |
| 26 | 1104 | 44.3 | 523 | 3 | AAY44994 | Aay44994 | HD70scFv- |
| 27 | 1098 | 44.0 | 239 | 7 | ADE28405 | Ade28405 | Human ant |
| 28 | 1097 | 44.0 | 238 | 8 | ADL93650 | Adl93650 | Human CD4 |
| 29 | 1097 | 44.0 | 239 | 7 | ADE28465 | Ade28465 | Human ant |
| 30 | 1095 | 43.9 | 238 | 8 | ADL93653 | Adl93653 | Human CD4 |
| 31 | 1094 | 43.9 | 238 | 8 | ADL93654 | Adl93654 | Human CD4 |
| 32 | 1093 | 43.8 | 239 | 7 | ADE28421 | Ade28421 | Human ant |
| 33 | 1093 | 43.8 | 239 | 7 | ADE28521 | Ade28521 | Human ant |
| 34 | 1092 | 43.8 | 239 | 7 | ADE28397 | Ade28397 | Human ant |
| 35 | 1090 | 43.7 | 239 | 7 | ADE28469 | Ade28469 | Human ant |
| 36 | 1090 | 43.7 | 239 | 7 | ADE28477 | Ade28477 | Human ant |
| 37 | 1088 | 43.6 | 219 | 7 | ADJ32150 | Adj32150 | Human int |
| 38 | 1088 | 43.6 | 238 | 8 | ADL93649 | Adl93649 | Human CD4 |
| 39 | 1082 | 43.4 | 238 | 8 | ADL93652 | Adl93652 | Human CD4 |
| 40 | 1079 | 43.3 | 239 | 7 | ADE28461 | Ade28461 | Human ant |
| 41 | 1077.5 | 43.2 | 237 | 8 | ADL93657 | Adl93657 | Human CD4 |
| 42 | 1077 | 43.2 | 239 | 3 | AAY82615 | Aay82615 | Human PTH |
| 43 | 1075.5 | 43.1 | 237 | 8 | ADL93658 | Adl93658 | Human CD4 |
| 44 | 1075.5 | 43.1 | 237 | 8 | ADL93651 | Adl93651 | Human CD4 |
| 45 | 1073 | 43.0 | 239 | 3 | AAY82616 | Aay82616 | Human PTH |

ALIGNMENTS

RESULT 1

ABJ38670

ID ABJ38670 standard; protein; 628 AA.

XX

AC ABJ38670;

XX

DT 26-JUN-2003 (first entry)

XX

DE Fab expression vector protein SEQ ID No 96.

XX

KW Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme;
KW antigen binding; receptor protein tyrosine kinase; skeletal dysplasia;
KW constitutive activation; craniosynostosis; cell proliferative disorder;
KW achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia;
KW hypochondroplasia; severe achondroplasia; transitional cell carcinoma;
KW Muenke coronal craniosynostosis; Crouzin syndrome; acanthosis nigricans;
KW tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma;
KW mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein;
KW Fab.

XX

OS Homo sapiens.

XX

PN WO2002102854-A2.

XX

PD 27-DEC-2002.

XX

PF 20-JUN-2002; 2002WO-IB003523.

XX

PR 20-JUN-2001; 2001US-0299187P.

XX

PA (MORP-) MORPHOSYS AG.

PA (PROC-) PROCHON BIOTECH LTD.

XX

PI Thomassen-Wolf E, Borges E, Yayon A, Rom E;

XX

DR WPI; 2003-167489/16.

XX

PT New molecules having the antigen-binding portion of antibodies that block
PT activation of receptor protein tyrosine kinase, useful for treating or
PT inhibiting skeletal dysplasias, craniosynostosis or cell proliferative
PT disorders.

XX

PS Disclosure; Fig 26B; 103pp; English.

XX

CC The invention relates to a novel molecule comprising the antigen binding
CC portion of an isolated antibody, which has an increased affinity for a
CC receptor protein tyrosine kinase and which blocks constitutive activation
CC of the receptor protein tyrosine kinase. The methods and compositions of
CC the invention are useful for treating or inhibiting a skeletal dysplasia,
CC craniosynostosis or a cell proliferative disorder. The skeletal dysplasia
CC is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe
CC achondroplasia with developmental delay or acanthosis nigricans
CC dysplasia. The craniosynostosis disorder is Muenke coronal
CC craniosynostosis or Crouzin syndrome with acanthosis nigricans. The cell
CC proliferative disorder is tumour progression that is progression of
CC transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple
CC myeloma or mammary carcinoma. This sequence represents the protein

CC derived from a Fab expression vector relating to the protein tyrosine
CC kinase inhibitor of the invention
XX
SQ Sequence 628 AA;

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 1.3e-132 | Length: | 628 |
| Score: | 1802.00 | Matches: | 370 |
| Percent Similarity: | 83.47% | Conservative: | 24 |
| Best Local Similarity: | 78.39% | Mismatches: | 52 |
| Query Match: | 72.25% | Indels: | 26 |
| DB: | 6 | Gaps: | 7 |

US-10-698-041-1 (1-1405) x ABJ38670 (1-628)

| | | | |
|----|-----|---------------------------------------------------------------|-----|
| Qy | 8 | CTGGCTGGTTTCGCTACCGTGGCCCAGGCGGCCGAGCTCGTGATGACTCAGTCTCCACTC | 67 |
| | | | |
| Db | 2 | LeuAlaGlyPheAlaThrValAlaGln---AlaAspIleValLeuThrGlnSerProAla | 20 |
| Qy | 68 | TCCCTGCCCCTCACCCTGGAGAGCCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTC | 127 |
| | | ::: | |
| Db | 21 | ThrLeuSerLeuSerProGlyGluArgAlaThrLeuSerCysArgAlaSerGlnSerVal | 40 |
| Qy | 128 | CTGCATAGTAATGGATACAACCTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCA | 187 |
| | | | |
| Db | 41 | SerSerSer-----TyrLeuAlaTrpTyrGlnGlnLysProGlyGlnAlaPro | 56 |
| Qy | 188 | CAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAAGTGGC | 247 |
| | | ::: | |
| Db | 57 | ArgLeuLeuIleTyrGlyAlaSerSerArgAlaThrGlyValProAlaArgPheSerGly | 76 |
| Qy | 248 | AGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGGAGGCTGAGGATGTTGGG | 307 |
| | | | |
| Db | 77 | SerGlySerGlyThrAspPheThrLeuThrIleSerSerLeuGluProGluAspPheAla | 96 |
| Qy | 308 | GTTTATTACTGCATGCAAGGTCTACAACTCCTAGGACCTTCGGCCAAGGGACACGACTG | 367 |
| | | | |
| Db | 97 | ValTyrTyrCysGlnGlnHisTyrThrThrProProThrPheGlyGlnGlyThrLysVal | 116 |
| Qy | 368 | GAGATTAAACGAACGTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAG | 427 |
| | | | |
| Db | 117 | GluIleLysArgThrValAlaAlaProSerValPheIlePheProProSerAspGluGln | 136 |
| Qy | 428 | TTGAAATCTGGAACCTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAGAGAGGCC | 487 |
| | | | |
| Db | 137 | LeuLysSerGlyThrAlaSerValValCysLeuLeuAsnAsnPheTyrProArgGluAla | 156 |
| Qy | 488 | AAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTAACTCCCAGGAGAGTGTACAC | 547 |
| | | | |
| Db | 157 | LysValGlnTrpLysValAspAsnAlaLeuGlnSerGlyAsnSerGlnGluSerValThr | 176 |
| Qy | 548 | GAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCACCTGACGCTGAGCAAAGCA | 607 |
| | | | |
| Db | 177 | GluGlnAspSerLysAspSerThrTyrSerLeuSerSerThrLeuThrLeuSerLysAla | 196 |
| Qy | 608 | GACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCCATCAGGGCCTGAGCTTGCCC | 667 |
| | | | |

Db 197 AspTyrGluLysHisLysValTyrAlaCysGluValThrHisGlnGlyLeuSerSerPro 216
 Qy 668 GTCACAAAGAGCTTCAACAGGGGAGAGTGTAGTTCTAGATAATTAATTAGGAGGAATTT 727
 ||||||||||||||||||
 Db 217 ValThrLysSerPheAsnArgGlyGluAla----- 226
 Qy 728 AAAATGAAATACCTATTGCCTACGGCAGCCGCTGGATTGTTATTACTCGCTGCCCAACCA 787
 ||||| ||| ||| ||||| ||| |||
 Db 227 ---MetLysGln-----SerThrIleAlaLeuAlaLeuLeuProLeuLeuPheThrPro 243
 Qy 788 ---GCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGGGGAGGCTTAGTTACGCCTGGGGGG 844
 ||||||||||||| ||||||||||||||||||
 Db 244 ValThrLysAlaGlnValGlnLeuValGluSerGlyGlyGlyLeuValGlnProGlyGly 263
 Qy 845 TCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACCTTCAGCAATTACTGGATGCACTGG 904
 ||||||||||||||| |||||||:::|||||||:::||| ||| |||
 Db 264 SerLeuArgLeuSerCysAlaAlaSerGlyPheThrPheSerSerTyrAlaMetSerTrp 283
 Qy 905 GTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTCTCACGTATTAATGAAGATGGGAGT 964
 ||||||||| ||||||||||||| |||||||| |||::: |||
 Db 284 ValArgGlnAlaProGlyLysGlyLeuGluTrpValSerAlaIleSerGlySerGlyGly 303
 Qy 965 ATCACAAACGACGCGGACTCCGTGAAGGGCCGATCCACCATCTCCAGAGACAACGCCAAG 1024
 ||| ||||||||||||||||| |||||||||||||||:::|||
 Db 304 SerThrTyrTyrAlaAspSerValLysGlyArgPheThrIleSerArgAspAsnSerLys 323
 Qy 1025 AACACGCTGTATCTGGAAATGAACAGTCTGAGAGCCGAGGACACGGCTGTCTATTACTGT 1084
 |||||||||||||:::||||||||||||||||||||
 Db 324 AsnThrLeuTyrLeuGlnMetAsnSerLeuArgAlaGluAspThrAlaValTyrTyrCys 343
 Qy 1085 ACACGAGATATTGGGGGTCGTGATGCT-----CACTGGGGGCCAGGGAACC 1129
 ||| ||| ||| ::|||
 Db 344 AlaArg-----TrpGlyGlyAspGlyPheTyrAlaMetAspTyrTrpGlyGlnGlyThr 361
 Qy 1130 CTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCCCTCC 1189
 ||||||||||||||||||||||||||||||||||
 Db 362 LeuValThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSer 381
 Qy 1190 TCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCCTGGTCAAGGACTACTTCCCC 1249
 ||||||||||||||||||||||||||||||||||
 Db 382 SerLysSerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPhePro 401
 Qy 1250 GAACCGGTGACGGTGTCTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCCG 1309
 ||||||||||||||||||||||||||||||||||
 Db 402 GluProValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPhePro 421
 Qy 1310 GCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGC 1369
 ||||||||||||||||||||||||||||||||||
 Db 422 AlaValLeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSer 441
 Qy 1370 AGCTTGGGACCCAGACCTACATCTGCAACGTGAAT 1405
 ||||||||||||||||||
 Db 442 SerLeuGlyThrGlnThrTyrIleCysAsnValAsn 453

us-10-698-041-1.n2p.rapb

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 14:34:27 ; Search time 165 Seconds
(without alignments)
5660.373 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 2843670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=x1h
-Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155503_6665/app_query.fasta_1.1543
-DB=Published_Applications_AA -QFMT=fastan -SUFFIX=n2p.rapb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US10698041_@CGN_1_1_128_@runat_14042005_155503_6665
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

us-10-698-041-1.n2p.rapb
 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|---------------------|-------------------|
| 1 | 1699.5 | 68.1 | 4852 | 15 | US-10-412-406-33 | Sequence 33, Appl |
| 2 | 1697.5 | 68.1 | 663 | 15 | US-10-412-406-32 | Sequence 32, Appl |
| 3 | 1668.5 | 66.9 | 491 | 13 | US-10-011-125-2 | Sequence 2, Appli |
| 4 | 1665.5 | 66.8 | 502 | 16 | US-10-679-620-88 | Sequence 88, Appl |
| 5 | 1664.5 | 66.7 | 512 | 16 | US-10-679-620-70 | Sequence 70, Appl |
| 6 | 1660 | 66.6 | 517 | 16 | US-10-679-620-68 | Sequence 68, Appl |
| 7 | 1658 | 66.5 | 519 | 16 | US-10-679-620-66 | Sequence 66, Appl |
| 8 | 1650 | 66.2 | 713 | 16 | US-10-679-620-64 | Sequence 64, Appl |
| 9 | 1648 | 66.1 | 715 | 16 | US-10-679-620-62 | Sequence 62, Appl |
| 10 | 1282.5 | 51.4 | 712 | 16 | US-10-679-620-116 | Sequence 116, App |
| 11 | 1178 | 47.2 | 483 | 16 | US-10-679-620-122 | Sequence 122, App |
| 12 | 1178 | 47.2 | 510 | 16 | US-10-679-620-74 | Sequence 74, Appl |
| 13 | 1178 | 47.2 | 510 | 16 | US-10-679-620-92 | Sequence 92, Appl |
| 14 | 1178 | 47.2 | 700 | 16 | US-10-679-620-94 | Sequence 94, Appl |
| 15 | 1142 | 45.8 | 219 | 16 | US-10-698-041-4 | Sequence 4, Appli |
| 16 | 1098 | 44.0 | 239 | 15 | US-10-292-088-16 | Sequence 16, Appl |
| 17 | 1097 | 44.0 | 238 | 16 | US-10-663-244-145 | Sequence 145, App |
| 18 | 1097 | 44.0 | 239 | 15 | US-10-292-088-56 | Sequence 56, Appl |
| 19 | 1095 | 43.9 | 238 | 16 | US-10-663-244-148 | Sequence 148, App |
| 20 | 1094 | 43.9 | 238 | 16 | US-10-663-244-149 | Sequence 149, App |
| 21 | 1093 | 43.8 | 239 | 15 | US-10-292-088-32 | Sequence 32, Appl |
| 22 | 1093 | 43.8 | 239 | 15 | US-10-292-088-102 | Sequence 102, App |
| 23 | 1092 | 43.8 | 239 | 15 | US-10-292-088-8 | Sequence 8, Appli |
| 24 | 1090 | 43.7 | 239 | 15 | US-10-292-088-64 | Sequence 64, Appl |
| 25 | 1090 | 43.7 | 239 | 15 | US-10-292-088-80 | Sequence 80, Appl |
| 26 | 1088 | 43.6 | 219 | 10 | US-09-972-656-104 | Sequence 104, App |
| 27 | 1088 | 43.6 | 238 | 16 | US-10-663-244-144 | Sequence 144, App |
| 28 | 1082 | 43.4 | 238 | 16 | US-10-663-244-147 | Sequence 147, App |
| 29 | 1079 | 43.3 | 239 | 15 | US-10-292-088-40 | Sequence 40, Appl |
| 30 | 1077.5 | 43.2 | 237 | 16 | US-10-663-244-152 | Sequence 152, App |
| 31 | 1075.5 | 43.1 | 237 | 16 | US-10-663-244-146 | Sequence 146, App |
| 32 | 1075.5 | 43.1 | 237 | 16 | US-10-663-244-153 | Sequence 153, App |
| 33 | 1067 | 42.8 | 239 | 15 | US-10-108-260A-4028 | Sequence 4028, Ap |
| 34 | 1060 | 42.5 | 239 | 10 | US-09-992-600A-8 | Sequence 8, Appli |
| 35 | 1060 | 42.5 | 239 | 10 | US-09-924-340-8 | Sequence 8, Appli |
| 36 | 1060 | 42.5 | 239 | 10 | US-09-992-095B-8 | Sequence 8, Appli |
| 37 | 1060 | 42.5 | 239 | 10 | US-09-999-570-8 | Sequence 8, Appli |
| 38 | 1060 | 42.5 | 239 | 14 | US-10-000-489-8 | Sequence 8, Appli |
| 39 | 1060 | 42.5 | 239 | 14 | US-10-000-986-8 | Sequence 8, Appli |
| 40 | 1060 | 42.5 | 239 | 14 | US-10-154-678-8 | Sequence 8, Appli |
| 41 | 1060 | 42.5 | 239 | 17 | US-10-838-854-8 | Sequence 8, Appli |
| 42 | 1052.5 | 42.2 | 220 | 9 | US-09-822-698A-24 | Sequence 24, Appl |
| 43 | 1048 | 42.0 | 247 | 15 | US-10-466-164-69 | Sequence 69, Appl |
| 44 | 1047 | 42.0 | 219 | 10 | US-09-972-656-106 | Sequence 106, App |
| 45 | 1044 | 41.9 | 239 | 15 | US-10-404-724-12 | Sequence 12, Appl |

RESULT 15
 US-10-698-041-4
 ; Sequence 4, Application US/10698041
 ; Publication No. US20040151724A1


```

; GENERAL INFORMATION:
; APPLICANT: Coronella-Wood, Julia
; TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer
; FILE REFERENCE: 5051.057
; CURRENT APPLICATION NUMBER: US/10/698,041
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/423,052
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-041-4

```

Alignment Scores:

| | | | |
|------------------------|----------|---------------|-----|
| Pred. No.: | 6.37e-69 | Length: | 219 |
| Score: | 1142.00 | Matches: | 219 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 45.79% | Indels: | 0 |
| DB: | 16 | Gaps: | 0 |

US-10-698-041-1 (1-1405) x US-10-698-041-4 (1-219)

```

Qy      41 GAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCC 100
      |||
Db      1 GluLeuValMetThrGlnSerProLeuSerLeuProValThrProGlyGluProAlaSer 20

Qy     101 ATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACTATTTGGATTGG 160
      |||
Db     21 IleSerCysArgSerSerGlnSerLeuLeuHisSerAsnGlyTyrAsnTyrLeuAspTrp 40

Qy     161 TACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCC 220
      |||
Db     41 TyrLeuGlnLysProGlyGlnSerProGlnLeuLeuIleTyrLeuGlyPheAsnArgAla 60

Qy     221 TCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTATACACTGAAAATC 280
      |||
Db     61 SerGlyValProAspArgPheSerGlySerGlySerGlyThrAspTyrThrLeuLysIle 80

Qy     281 AGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTCTACAACTCCT 340
      |||
Db     81 SerArgValGluAlaGluAspValGlyValTyrTyrCysMetGlnGlyLeuGlnThrPro 100

Qy     341 AGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAACTGTGGCTGCACCATCTGTC 400
      |||
Db    101 ArgThrPheGlyGlnGlyThrArgLeuGluIleLysArgThrValAlaAlaProSerVal 120

Qy     401 TTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTG 460
      |||
Db    121 PheIlePheProProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCysLeu 140

Qy     461 CTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGAAGGTGGATAACGCCCTCCAA 520
      |||
Db    141 LeuAsnAsnPheTyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeuGln 160

Qy     521 TCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTC 580
      |||
Db    161 SerGlyAsnSerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSerLeu 180

Qy     581 AGCAGCACCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAA 640

```

us-10-698-041-1.n2p.rapb

```
Db      181 SerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCysGlu 200
Qy      641 GTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT 697
Db      201 ValThrHisGlnGlyLeuSerLeuProValThrLysSerPheAsnArgGlyGluCys 219
```

Search completed: April 15, 2005, 14:54:48
Job time : 190 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 14:02:16 ; Search time 31.5 Seconds
(without alignments)
8583.146 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh

Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155501_6556/app_query.fasta_1.15
43

-DB=PIR_79 -QFMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10698041@CGN_1_1_37@runat_14042005_155501_6556 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result | % | | | | | Description |
|--------|-------|-------|-------|--------|--------|--------------------|
| | No. | Score | Match | Length | ID | |
| 1 | 897 | 36.0 | 215 | 2 | JE0242 | Ig kappa chain NIG |
| 2 | 874 | 35.0 | 215 | 2 | JE0244 | Ig kappa chain NIG |
| 3 | 856 | 34.3 | 215 | 2 | JE0243 | Ig kappa chain NIG |
| 4 | 848.5 | 34.0 | 216 | 2 | JE0241 | Ig kappa chain Am3 |
| 5 | 843 | 33.8 | 215 | 2 | A23746 | Ig kappa chain V-I |
| 6 | 800 | 32.1 | 219 | 2 | S52028 | Ig kappa chain - m |
| 7 | 800 | 32.1 | 219 | 2 | PC4203 | Ig kappa chain (mo |
| 8 | 789 | 31.6 | 219 | 2 | S16112 | Ig kappa chain V r |
| 9 | 785 | 31.5 | 219 | 2 | S38865 | Ig kappa chain - m |
| 10 | 778 | 31.2 | 217 | 2 | S42772 | Ig kappa chain - m |
| 11 | 756 | 30.3 | 225 | 2 | JL0029 | Ig kappa chain pre |
| 12 | 741.5 | 29.7 | 240 | 2 | S06084 | Ig kappa chain pre |
| 13 | 728 | 29.2 | 220 | 2 | A49444 | Ig gamma-1 heavy c |
| 14 | 702.5 | 28.2 | 220 | 2 | A31790 | Ig kappa chain V r |
| 15 | 693.5 | 27.8 | 218 | 2 | S68241 | Ig kappa chain V r |
| 16 | 680.5 | 27.3 | 218 | 2 | JC5810 | monoclonal antibod |
| 17 | 677.5 | 27.2 | 214 | 2 | S68212 | Ig kappa chain (Ma |
| 18 | 665 | 26.7 | 548 | 2 | S38864 | Ig epsilon chain C |
| 19 | 660.5 | 26.5 | 241 | 2 | S69131 | Ig heavy chain (DO |
| 20 | 655.5 | 26.3 | 210 | 2 | A56169 | Ig kappa chain V r |
| 21 | 655.5 | 26.3 | 213 | 2 | S68213 | Ig heavy chain (Ma |
| 22 | 655.5 | 26.3 | 234 | 2 | S01320 | Ig kappa chain pre |
| 23 | 655 | 26.3 | 197 | 2 | S29593 | Ig kappa chain (WM |
| 24 | 649.5 | 26.0 | 230 | 2 | S33161 | Ig kappa chain - s |
| 25 | 646.5 | 25.9 | 234 | 2 | S14237 | Ig kappa chain pre |
| 26 | 639.5 | 25.6 | 225 | 2 | S37484 | Ig kappa chain - m |
| 27 | 633 | 25.4 | 178 | 2 | PT0219 | Ig kappa chain V-C |
| 28 | 627 | 25.1 | 235 | 2 | S25058 | Ig kappa chain - m |
| 29 | 626 | 25.1 | 444 | 2 | PC4436 | monoclonal antibod |
| 30 | 621 | 24.9 | 220 | 2 | S68211 | Ig heavy chain (Ma |
| 31 | 600.5 | 24.1 | 254 | 2 | B31790 | Ig heavy chain V r |
| 32 | 598.5 | 24.0 | 246 | 2 | S38950 | Ig gamma chain - m |
| 33 | 598.5 | 24.0 | 446 | 2 | S40295 | Ig gamma-2a chain |
| 34 | 594 | 23.8 | 135 | 2 | S40342 | Ig kappa chain - h |
| 35 | 594 | 23.8 | 135 | 2 | S52059 | JC-kappa protein - |
| 36 | 593.5 | 23.8 | 469 | 2 | S37483 | Ig gamma-2a chain |
| 37 | 593 | 23.8 | 121 | 2 | S40371 | Ig kappa chain - h |
| 38 | 592 | 23.7 | 474 | 1 | G2MS11 | Ig gamma-2b chain |
| 39 | 576 | 23.1 | 214 | 2 | PC4202 | monoclonal antibod |
| 40 | 571 | 22.9 | 136 | 2 | S40357 | Ig kappa chain V-J |
| 41 | 570.5 | 22.9 | 221 | 2 | S49220 | Ig gamma-1 chain - |
| 42 | 565 | 22.7 | 470 | 2 | S22080 | Ig heavy chain pre |
| 43 | 560 | 22.5 | 117 | 1 | K2HUGM | Ig kappa chain pre |
| 44 | 559 | 22.4 | 143 | 2 | S23624 | Ig heavy chain V r |
| 45 | 557 | 22.3 | 132 | 2 | S26882 | Ig kappa chain V r |

us-10-698-041-1.n2p.rup

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 12:25:16 ; Search time 145.5 Seconds
(without alignments)
9889.639 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155501_6542/app_query.fasta_1.1543
-DB=UniProt_03 -QFMT=fastan -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10698041_@CGN_1_1_197_@runat_14042005_155501_6542 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|--------|--------------------|
| 1 | 1097 | 44.0 | 239 | 2 | Q8NEK0 | Q8nek0 homo sapien |
| 2 | 1070.5 | 42.9 | 240 | 2 | Q6PIH6 | Q6pih6 homo sapien |
| 3 | 992 | 39.8 | 239 | 2 | Q8TCD0 | Q8tcd0 homo sapien |
| 4 | 992 | 39.8 | 239 | 2 | Q6P491 | Q6p491 homo sapien |
| 5 | 904.5 | 36.3 | 236 | 2 | Q6PIL8 | Q6pil8 homo sapien |
| 6 | 888 | 35.6 | 235 | 2 | Q6GMV9 | Q6gmv9 homo sapien |

| | | | | | | | |
|----|-------|------|-----|-------------------------|--------|--------|-------------|
| | | | | us-10-698-041-1.n2p.rup | | | |
| 7 | 888 | 35.6 | 470 | 2 | Q6PJA4 | Q6pja4 | homo sapien |
| 8 | 878 | 35.2 | 235 | 2 | Q6PJF2 | Q6pjf2 | homo sapien |
| 9 | 877.5 | 35.2 | 236 | 2 | Q6P5S8 | Q6p5s8 | homo sapien |
| 10 | 876 | 35.1 | 478 | 2 | Q6PI81 | Q6pi81 | homo sapien |
| 11 | 873.5 | 35.0 | 466 | 2 | Q6N096 | Q6n096 | homo sapien |
| 12 | 865 | 34.7 | 235 | 2 | Q6GMW0 | Q6gmw0 | homo sapien |
| 13 | 864.5 | 34.7 | 472 | 2 | Q6N089 | Q6n089 | homo sapien |
| 14 | 852.5 | 34.2 | 236 | 2 | Q6GMW1 | Q6gmw1 | homo sapien |
| 15 | 852 | 34.2 | 465 | 2 | Q6P6C4 | Q6p6c4 | homo sapien |
| 16 | 849.5 | 34.1 | 234 | 2 | Q7Z473 | Q7z473 | homo sapien |
| 17 | 846.5 | 33.9 | 236 | 2 | Q6GMX0 | Q6gmx0 | homo sapien |
| 18 | 845 | 33.9 | 466 | 2 | Q6IN78 | Q6in78 | homo sapien |
| 19 | 842.5 | 33.8 | 473 | 2 | Q6MZV7 | Q6mzv7 | homo sapien |
| 20 | 838.5 | 33.6 | 236 | 2 | Q6GMX8 | Q6gmx8 | homo sapien |
| 21 | 838.5 | 33.6 | 236 | 2 | Q7Z3Y4 | Q7z3y4 | homo sapien |
| 22 | 836 | 33.5 | 544 | 2 | Q6PJ95 | Q6pj95 | homo sapien |
| 23 | 835.5 | 33.5 | 236 | 2 | Q6PIT5 | Q6pit5 | homo sapien |
| 24 | 835 | 33.5 | 236 | 2 | Q6ZP85 | Q6zp85 | homo sapien |
| 25 | 834 | 33.4 | 475 | 2 | Q6MZQ6 | Q6mzq6 | homo sapien |
| 26 | 833.5 | 33.4 | 236 | 2 | Q6PIH7 | Q6pih7 | homo sapien |
| 27 | 829.5 | 33.3 | 464 | 2 | Q6MZU6 | Q6mzu6 | homo sapien |
| 28 | 827 | 33.2 | 470 | 2 | Q7Z5W1 | Q7z5w1 | homo sapien |
| 29 | 818.5 | 32.8 | 236 | 2 | Q6GMX9 | Q6gmx9 | homo sapien |
| 30 | 815.5 | 32.7 | 475 | 2 | Q6GMW7 | Q6gmw7 | homo sapien |
| 31 | 812 | 32.6 | 473 | 2 | Q6P055 | Q6p055 | homo sapien |
| 32 | 808.5 | 32.4 | 236 | 2 | Q6PIH4 | Q6pih4 | homo sapien |
| 33 | 807 | 32.4 | 480 | 2 | Q6N094 | Q6n094 | homo sapien |
| 34 | 792.5 | 31.8 | 521 | 2 | Q8N4Y9 | Q8n4y9 | homo sapien |
| 35 | 789 | 31.6 | 219 | 2 | Q65ZC0 | Q65zc0 | mus musculu |
| 36 | 785.5 | 31.5 | 482 | 2 | Q7Z351 | Q7z351 | homo sapien |
| 37 | 772 | 31.0 | 475 | 2 | Q6N095 | Q6n095 | homo sapien |
| 38 | 765 | 30.7 | 481 | 2 | Q6N097 | Q6n097 | homo sapien |
| 39 | 761.5 | 30.5 | 465 | 2 | Q6GMX6 | Q6gmx6 | homo sapien |
| 40 | 759 | 30.4 | 493 | 2 | Q68CN4 | Q68cn4 | homo sapien |
| 41 | 741 | 29.7 | 476 | 2 | Q6GMX1 | Q6gmx1 | homo sapien |
| 42 | 736.5 | 29.5 | 518 | 2 | Q6N030 | Q6n030 | homo sapien |
| 43 | 734.5 | 29.5 | 469 | 2 | Q7Z7P5 | Q7z7p5 | homo sapien |
| 44 | 725 | 29.1 | 480 | 2 | Q6PJF1 | Q6pjf1 | homo sapien |
| 45 | 702 | 28.1 | 417 | 2 | Q6N093 | Q6n093 | homo sapien |

us-10-698-041-1.rni

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 08:20:56 ; Search time 263 Seconds
(without alignments)
8741.326 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|-------|---------------|--------|----|-------------------|-------------------|
| 1 | 958.4 | 68.2 | 5925 | 4 | US-09-315-926A-78 | Sequence 78, Appl |
| 2 | 901.4 | 64.2 | 4691 | 3 | US-08-591-632-43 | Sequence 43, Appl |
| 3 | 901.4 | 64.2 | 4691 | 3 | US-09-611-451-43 | Sequence 43, Appl |
| 4 | 901.4 | 64.2 | 6166 | 3 | US-08-591-632-51 | Sequence 51, Appl |
| 5 | 901.4 | 64.2 | 6166 | 3 | US-09-611-451-51 | Sequence 51, Appl |
| 6 | 779.8 | 55.5 | 6563 | 3 | US-09-027-449-61 | Sequence 61, Appl |
| 7 | 779.8 | 55.5 | 6563 | 3 | US-08-804-444A-61 | Sequence 61, Appl |
| 8 | 779.8 | 55.5 | 6563 | 3 | US-09-026-985-61 | Sequence 61, Appl |
| 9 | 779.8 | 55.5 | 6563 | 3 | US-09-121-952A-61 | Sequence 61, Appl |
| 10 | 779.8 | 55.5 | 6563 | 3 | US-09-234-340A-61 | Sequence 61, Appl |
| 11 | 747.4 | 53.2 | 2178 | 1 | US-08-463-587A-24 | Sequence 24, Appl |
| 12 | 747.4 | 53.2 | 2178 | 2 | US-08-463-667A-2 | Sequence 2, Appli |
| 13 | 747.4 | 53.2 | 2178 | 3 | US-08-923-854-24 | Sequence 24, Appl |
| 14 | 747.4 | 53.2 | 2178 | 5 | PCT-US91-09133-25 | Sequence 25, Appl |
| 15 | 739.6 | 52.6 | 1951 | 4 | US-10-011-125A-1 | Sequence 1, Appli |
| 16 | 738.6 | 52.6 | 2143 | 3 | US-09-097-309-5 | Sequence 5, Appli |
| 17 | 738.6 | 52.6 | 2143 | 3 | US-09-097-171A-9 | Sequence 9, Appli |

| | | | | | us-10-698-041-1.rni | |
|----|-------|------|------|---|---------------------|-------------------|
| 18 | 738.6 | 52.6 | 2143 | 3 | US-09-460-587-5 | Sequence 5, Appli |
| 19 | 738.6 | 52.6 | 2143 | 4 | US-09-940-166A-5 | Sequence 5, Appli |
| 20 | 738.6 | 52.6 | 6550 | 3 | US-09-422-712B-1 | Sequence 1, Appli |
| 21 | 738.6 | 52.6 | 6550 | 3 | US-09-607-756-1 | Sequence 1, Appli |
| 22 | 734.6 | 52.3 | 6127 | 2 | US-08-887-352B-1 | Sequence 1, Appli |
| 23 | 734.6 | 52.3 | 6127 | 3 | US-09-109-207C-1 | Sequence 1, Appli |
| 24 | 734.6 | 52.3 | 6127 | 3 | US-09-296-005-1 | Sequence 1, Appli |
| 25 | 734.6 | 52.3 | 6127 | 4 | US-09-920-171-1 | Sequence 1, Appli |
| 26 | 734.6 | 52.3 | 6127 | 4 | US-09-716-028-1 | Sequence 1, Appli |
| 27 | 734.6 | 52.3 | 6127 | 4 | US-10-113-996-1 | Sequence 1, Appli |
| 28 | 632.2 | 45.0 | 3169 | 3 | US-08-630-820-5 | Sequence 5, Appli |
| 29 | 632.2 | 45.0 | 3169 | 4 | US-09-273-453-5 | Sequence 5, Appli |
| 30 | 604.6 | 43.0 | 968 | 4 | US-10-000-489-7 | Sequence 7, Appli |
| 31 | 566.4 | 40.3 | 1632 | 2 | US-08-792-824-8 | Sequence 8, Appli |
| 32 | 566.4 | 40.3 | 1644 | 2 | US-08-792-824-11 | Sequence 11, Appl |
| 33 | 564.8 | 40.2 | 1672 | 2 | US-08-792-824-2 | Sequence 2, Appli |
| 34 | 564.8 | 40.2 | 4435 | 2 | US-08-792-824-1 | Sequence 1, Appli |
| 35 | 542.8 | 38.6 | 720 | 3 | US-08-487-550-5 | Sequence 5, Appli |
| 36 | 542.8 | 38.6 | 720 | 4 | US-09-526-098-5 | Sequence 5, Appli |
| 37 | 542.8 | 38.6 | 720 | 4 | US-09-383-916-5 | Sequence 5, Appli |
| 38 | 542.4 | 38.6 | 1641 | 2 | US-08-792-824-5 | Sequence 5, Appli |
| 39 | 522.8 | 37.2 | 729 | 1 | US-08-398-613A-55 | Sequence 55, Appl |
| 40 | 522.8 | 37.2 | 729 | 1 | US-08-398-612A-55 | Sequence 55, Appl |
| 41 | 522.8 | 37.2 | 729 | 1 | US-08-398-611A-55 | Sequence 55, Appl |
| 42 | 522.8 | 37.2 | 729 | 1 | US-08-396-851A-55 | Sequence 55, Appl |
| 43 | 522.8 | 37.2 | 729 | 2 | US-08-491-334A-55 | Sequence 55, Appl |
| 44 | 522.8 | 37.2 | 729 | 3 | US-09-027-449-41 | Sequence 41, Appl |
| 45 | 522.8 | 37.2 | 729 | 3 | US-08-804-444A-41 | Sequence 41, Appl |

ALIGNMENTS

```

RESULT 1
US-09-315-926A-78
; Sequence 78, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Es van, Helmut
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 78
; LENGTH: 5925
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: phage
; NAME/KEY: primer_bind
; LOCATION: (1)..(5925)
; OTHER INFORMATION: /note="Nucleotide hCAT1 encoding sequence
US-09-315-926A-78

```


us-10-698-041-1.rni

Query Match 68.2%; Score 958.4; DB 4; Length 5925;
 Best Local Similarity 83.5%; Pred. No. 1.2e-257;
 Matches 1147; Conservative 0; Mismatches 196; Indels 31; Gaps 4;

```

Qy      51 TGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCCTCCATCTCCTGCA 110
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2339 TCACGCAGTCTCCAGGCATCCTGTCTTTGTCTCCGGGGGCAGGAGCCACCCTCTCCTGCA 2398

Qy      111 GGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACTATTTGGATTGGTACCTGCAGA 170
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2399 GGGCCAGTCAGAGTGTGAGCAGCAGGAAC-----TTAGCCTGGTACCAGCAGA 2446

Qy      171 AGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGGGCCTCCGGGGTCC 230
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2447 AACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGTGTATCCAACAGGGCCACTGGCGTCC 2506

Qy      231 CTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTATACACTGAAAATCAGCAGAGTGG 290
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2507 CAGACAGGTTCACTGGCAGTGGGTCTGGGGCAGACTTCACTCTCACCATCAACAGACTGG 2566

Qy      291 AGGCTGAGGATGTTGGGGTTTTACTGTCATGCAAGGTCTACAACTCCTAGGACCTTCG 350
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2567 AGCCTGAAGATTTTGCAGGTGATTACTGTGAGCGGTATGGCAGGTCACTGTGGACGTTTCG 2626

Qy      351 GCCAAGGGACACGACTGGAGATTAAC---GAACTGTGGCTGCACCATCTGTCTTCATCT 407
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2627 GTCAAGGGACCAAGGTGGAGATCAAACGTGGAAGTGTGGCTGCACCATCTGTCTTCATCT 2686

Qy      408 TCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATA 467
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2687 TCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGCCTGCTGAATA 2746

Qy      468 ACTTCTATCCCAGAGAGGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTA 527
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2747 ACTTCTATCCCAGAGAGGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTCCAATCGGGTA 2806

Qy      528 ACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA 587
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2807 ACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCAGCAGCA 2866

Qy      588 CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC 647
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2867 CCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGCGAAGTCACCC 2926

Qy      648 ATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGTTA-----G 700
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2927 ATCAGGGCCTGAGTTCAACGGTGACAAAGAGCTTCAACAGGGGAGAGTGTTAATAAGGCG 2986

Qy      701 TTCTAGATAATTAATTAGGAGGAATTTAAATGAAATACCTATTGCCTACGGCAGCCGCT 760
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      2987 CGCCAATTCTATTTCAAGGAGACAGTCATAATGAAATACCTATTGCCTACGGCAGCCGCT 3046

Qy      761 GGATTGTTATTACTCGCTGCCCAACCAGCCATGGCCCAGGTGCAGCTGCAGGAGTCCGGG 820
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3047 GGATTGTTATTACTCGCGGGCCAGCCGGCCATGGCCCAGGTCCAGCTGGTGCAGTCTGGG 3106

Qy      821 GGAGGCTTAGTTGAGCCTGGGGGGTCCCTGAGACTCTCCTGTGAAGCCTCTGGATACACC 880
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3107 GGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGAGCCTCTGGATTACCC 3166

Qy      881 TTCAGCAATTAAGTGCAGTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTGTGGGTC 940
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      3167 TTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGGGTG 3226

```

us-10-698-041-1.rni

| | | | |
|----|------|---------------------------------------------------------------|------|
| Qy | 941 | TCACGTATTAATGAAGATGGGAGTATCACAAACGACGCGGACTCCGTGAAGGGCCGATCC | 1000 |
| Db | 3227 | GCAGTTATATCATATGATGGAAGCAATAAATACTACGCAGACTCCGTGAAGGGCCGATTC | 3286 |
| Qy | 1001 | ACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGAAAATGAACAGTCTGAGAGCC | 1060 |
| Db | 3287 | ACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGAGCT | 3346 |
| Qy | 1061 | GAGGACACGGCTGTCTATTACTGTACACGAGATATTGGGG-----GTCGTGATGCT | 1111 |
| Db | 3347 | GAGGACACGGCTGTGTATTACTGTGCGAGAGGGATTACAGTAACTAAATCACGATTTGAC | 3406 |
| Qy | 1112 | CACTGGGGCCAGGGAACCCCTGGTCACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTC | 1171 |
| Db | 3407 | TACTGGGGCCAGGGCACCCCTGGTCACCGTCTCAAGCGCCTCCACCAAGGGCCCATCGGTC | 3466 |
| Qy | 1172 | TTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG | 1231 |
| Db | 3467 | TTCCCCCTGGCACCCCTCCTCCAAGAGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTG | 3526 |
| Qy | 1232 | GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGC | 1291 |
| Db | 3527 | GTCAAGGACTACTTCCCCGAACCGGTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGC | 3586 |
| Qy | 1292 | GGCGTGACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTG | 1351 |
| Db | 3587 | GGCGTCCACACCTTCCCGGCTGTCCTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTA | 3646 |
| Qy | 1352 | GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT | 1405 |
| Db | 3647 | GTGACCGTGCCCTCCAGCAGCTTGGGCACCCAGACCTACATCTGCAACGTGAAT | 3700 |

us-10-698-041-1.n2p.ra1

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 15, 2005, 14:10:36 ; Search time 27.5 Seconds
(without alignments)
7627.777 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 2494
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delect 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODEL=frame+_n2p.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US10698041/runat_14042005_155502_6573/app_query.fasta_1.1543
-DB=Issued_Patents_AA -QFMT=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10698041_@CGN_1_1_30_@runat_14042005_155502_6573 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|------------------|-------------------|
| 1 | 1668.5 | 66.9 | 491 | 4 | US-10-011-125A-2 | Sequence 2, Appli |
| 2 | 1060 | 42.5 | 239 | 4 | US-10-000-489-8 | Sequence 8, Appli |

| | | | | us-10-698-041-1.n2p.ra1 | | |
|----|--------|------|-----|-------------------------|-------------------|-------------------|
| 3 | 1005.5 | 40.3 | 239 | 3 | US-08-487-550-6 | Sequence 6, Appli |
| 4 | 1005.5 | 40.3 | 239 | 4 | US-09-526-098-6 | Sequence 6, Appli |
| 5 | 1005.5 | 40.3 | 239 | 4 | US-09-383-916-6 | Sequence 6, Appli |
| 6 | 982.5 | 39.4 | 248 | 4 | US-09-315-926A-80 | Sequence 80, Appl |
| 7 | 979 | 39.3 | 238 | 4 | US-09-698-705-10 | Sequence 10, Appl |
| 8 | 960 | 38.5 | 242 | 1 | US-08-398-613A-56 | Sequence 56, Appl |
| 9 | 960 | 38.5 | 242 | 1 | US-08-398-612A-56 | Sequence 56, Appl |
| 10 | 960 | 38.5 | 242 | 1 | US-08-398-611A-56 | Sequence 56, Appl |
| 11 | 960 | 38.5 | 242 | 2 | US-08-491-334A-56 | Sequence 56, Appl |
| 12 | 960 | 38.5 | 242 | 3 | US-09-027-449-42 | Sequence 42, Appl |
| 13 | 960 | 38.5 | 242 | 3 | US-08-804-444A-42 | Sequence 42, Appl |
| 14 | 960 | 38.5 | 242 | 3 | US-09-026-985-42 | Sequence 42, Appl |
| 15 | 960 | 38.5 | 242 | 4 | US-09-121-952A-42 | Sequence 42, Appl |
| 16 | 960 | 38.5 | 242 | 4 | US-09-234-340A-42 | Sequence 42, Appl |
| 17 | 951.5 | 38.2 | 218 | 4 | US-09-698-705-12 | Sequence 12, Appl |
| 18 | 927 | 37.2 | 599 | 1 | US-08-442-542-18 | Sequence 18, Appl |
| 19 | 927 | 37.2 | 599 | 3 | US-08-765-469-18 | Sequence 18, Appl |
| 20 | 915.5 | 36.7 | 240 | 4 | US-09-301-593-36 | Sequence 36, Appl |
| 21 | 907 | 36.4 | 241 | 2 | US-07-916-098A-56 | Sequence 56, Appl |
| 22 | 904 | 36.2 | 242 | 3 | US-09-027-449-51 | Sequence 51, Appl |
| 23 | 904 | 36.2 | 242 | 3 | US-09-027-449-56 | Sequence 56, Appl |
| 24 | 904 | 36.2 | 242 | 3 | US-09-027-449-62 | Sequence 62, Appl |
| 25 | 904 | 36.2 | 242 | 3 | US-08-804-444A-51 | Sequence 51, Appl |
| 26 | 904 | 36.2 | 242 | 3 | US-08-804-444A-56 | Sequence 56, Appl |
| 27 | 904 | 36.2 | 242 | 3 | US-09-026-985-51 | Sequence 51, Appl |
| 28 | 904 | 36.2 | 242 | 3 | US-09-026-985-56 | Sequence 56, Appl |
| 29 | 904 | 36.2 | 242 | 3 | US-09-026-985-62 | Sequence 62, Appl |
| 30 | 904 | 36.2 | 242 | 4 | US-09-121-952A-51 | Sequence 51, Appl |
| 31 | 904 | 36.2 | 242 | 4 | US-09-121-952A-56 | Sequence 56, Appl |
| 32 | 904 | 36.2 | 242 | 4 | US-09-121-952A-62 | Sequence 62, Appl |
| 33 | 904 | 36.2 | 242 | 4 | US-09-234-340A-51 | Sequence 51, Appl |
| 34 | 904 | 36.2 | 242 | 4 | US-09-234-340A-56 | Sequence 56, Appl |
| 35 | 904 | 36.2 | 242 | 4 | US-09-234-340A-62 | Sequence 62, Appl |
| 36 | 902.5 | 36.2 | 220 | 3 | US-08-952-235-1 | Sequence 1, Appli |
| 37 | 902.5 | 36.2 | 220 | 4 | US-09-669-971-1 | Sequence 1, Appli |
| 38 | 902 | 36.2 | 239 | 4 | US-09-627-896B-22 | Sequence 22, Appl |
| 39 | 900.5 | 36.1 | 226 | 4 | US-09-456-090A-86 | Sequence 86, Appl |
| 40 | 900.5 | 36.1 | 226 | 4 | US-09-453-234-86 | Sequence 86, Appl |
| 41 | 900 | 36.1 | 219 | 3 | US-09-027-449-72 | Sequence 72, Appl |
| 42 | 900 | 36.1 | 219 | 3 | US-09-026-985-72 | Sequence 72, Appl |
| 43 | 900 | 36.1 | 219 | 4 | US-09-121-952A-72 | Sequence 72, Appl |
| 44 | 900 | 36.1 | 219 | 4 | US-09-234-340A-72 | Sequence 72, Appl |
| 45 | 900 | 36.1 | 235 | 4 | US-09-472-087-14 | Sequence 14, Appl |

ALIGNMENTS

```

RESULT 1
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
;   APPLICANT: Chen, Christina Yu-Ching
;   TITLE OF INVENTION: BACTERIAL HOST STRAINS
;   FILE REFERENCE: P1804R1
;   CURRENT APPLICATION NUMBER: US/10/011,125A
;   CURRENT FILING DATE: 2001-12-07
;   PRIOR APPLICATION NUMBER: US 60/256,162
;   PRIOR FILING DATE: 2000-12-14
;   NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
;   LENGTH: 491
;   TYPE: PRT

```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
US-10-011-125A-2

```

| | | | |
|------------------------|-----------|---------------|-----|
| Pred. No.: | 1.23e-133 | Length: | 491 |
| Score: | 1668.50 | Matches: | 340 |
| Percent Similarity: | 78.94% | Conservative: | 31 |
| Best Local Similarity: | 72.34% | Mismatches: | 62 |
| Query Match: | 66.90% | Indels: | 37 |
| DB: | 4 | Gaps: | 7 |

| | | | |
|----|-----|---------------------------------------------------------------|-----|
| Qy | 38 | GCCGAGCTCGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAGCCGGCC | 97 |
| Db | 23 | AlaAspIleGlnLeuThrGlnSerProSerSerLeuSerAlaSerValGlyAspArgVal | 42 |
| Qy | 98 | TCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGATACAACCTATTTGGAT | 157 |
| Db | 43 | ThrIleThrCysSerAlaSerGlnAspIle-----SerAsnTyrLeuAsn | 57 |
| Qy | 158 | TGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTCCTGATCTATTTGGGTTTTAATCGG | 217 |
| Db | 58 | TrpTyrGlnGlnLysProGlyLysAlaProLysLeuLeuIleTyrPheThrSerSerLeu | 77 |
| Qy | 218 | GCCTCCGGGGTCCCTGACAGGTTCACTGGCAGTGGATCAGGCACAGATTATACACTGAAA | 277 |
| Db | 78 | HisSerGlyValProSerArgPheSerGlySerGlySerGlyThrAspTyrThrLeuThr | 97 |
| Qy | 278 | ATCAGCAGAGTGGAGGCTGAGGATGTTGGGGTTTATTACTGCATGCAAGGTCTACAACT | 337 |
| Db | 98 | IleSerSerLeuGlnProGluAspPheAlaThrTyrTyrCysGlnGlnTyrSerThrVal | 117 |
| Qy | 338 | CCTAGGACCTTCGGCCAAGGGACACGACTGGAGATTAAACGAAGTGTGGCTGCACCATCT | 397 |
| Db | 118 | ProTrpThrPheGlyGlnGlyThrLysValGluIleLysArgThrValAlaAlaProSer | 137 |
| Qy | 398 | GTCTTCATCTTCCCGCCATCTGATGAGCAGTTGAAATCTGGAAGTGCCTCTGTTGTGTGC | 457 |
| Db | 138 | ValPheIlePheProProSerAspGluGlnLeuLysSerGlyThrAlaSerValValCys | 157 |
| Qy | 458 | CTGCTGAATAACTTCTATCCCAGAGAGGCCAAAGTACAGTGGAAAGGTGGATAACGCCCTC | 517 |
| Db | 158 | LeuLeuAsnAsnPheTyrProArgGluAlaLysValGlnTrpLysValAspAsnAlaLeu | 177 |
| Qy | 518 | CAATCGGGTAACTCCCAGGAGAGTGTACAGAGCAGGACAGCAAGGACAGCACCTACAGC | 577 |
| Db | 178 | GlnSerGlyAsnSerGlnGluSerValThrGluGlnAspSerLysAspSerThrTyrSer | 197 |
| Qy | 578 | CTCAGCAGCACCCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACGCCTGC | 637 |
| Db | 198 | LeuSerSerThrLeuThrLeuSerLysAlaAspTyrGluLysHisLysValTyrAlaCys | 217 |
| Qy | 638 | GAAGTCACCCATCAGGGCCTGAGCTTGCCCGTCACAAAGAGCTTCAACAGGGGAGAGTGT | 697 |
| Db | 218 | GluValThrHisGlnGlyLeuSerSerProValThrLysSerPheAsnArgGlyGluCys | 237 |
| Qy | 698 | TAGTTCTAGATAATTAATTAGGAGGAATTTAAATGAAATACCTATTGCCTACGGCAGCC | 757 |
| Db | 238 | -----MetLysLysAsnIleAlaPheLeuLeu | 246 |

us-10-698-041-1.n2p.raii

| | | | |
|----|------|--------------------------------------------------------------|------|
| Qy | 758 | GCTGGATTGTTATTACTCGCT---GCCCAACAGCCATGGCCCCAGGTGCAGTGCAGGAG | 814 |
| Db | 247 | AlaSerMetPheValPheSerIleAlaThrAsnAlaTyrAlaGluValGlnLeuValGlu | 266 |
| Qy | 815 | TCCGGGGGAGGCTTAGTTAGCCTGGGGGGTCCCTGAGACTCTCTGTGAAGCCTCTGGA | 874 |
| Db | 267 | SerGlyGlyGlyLeuValGlnProGlyGlySerLeuArgLeuSerCysAlaAlaSerGly | 286 |
| Qy | 875 | TACACCTTCAGCAATTACTGGATGCACTGGGTCCGCCAACCTCCAGGGAAGGGGCTGGTG | 934 |
| Db | 287 | TyrThrPheThrAsnTyrGlyMetAsnTrpIleArgGlnAlaProGlyLysGlyLeuGlu | 306 |
| Qy | 935 | TGGGTCTCACGTATTAATGAA---GATGGGAGTATCACAAACGACGCGGACTCCGTGAAG | 991 |
| Db | 307 | TrpValGlyTrpIleAsnThrTyrThrGlyGluProThrTyrAlaAlaAsp---PheLys | 325 |
| Qy | 992 | GGCCGATCCACCATCTCCAGAGACAACGCCAAGAACACGCTGTATCTGGAAATGAACAGT | 1051 |
| Db | 326 | ArgArgPheThrIleSerAlaAspThrSerSerAsnThrValTyrLeuGlnMetAsnSer | 345 |
| Qy | 1052 | CTGAGAGCCGAGGACACGGCTGTCTATTACTGTACACGA----- | 1090 |
| Db | 346 | LeuArgAlaGluAspThrAlaValTyrTyrCysAlaLysTyrProHisTyrTyrGlySer | 365 |
| Qy | 1091 | -----GATATTGGGGGTCGTGATGCTCACTGGGGCCAGGGAACCCTGGTC | 1135 |
| Db | 366 | SerHisTrpTyrPheAspVal-----TrpGlyGlnGlyThrLeuVal | 379 |
| Qy | 1136 | ACCGTCTCCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCTGGCACCTCCTCCAAG | 1195 |
| Db | 380 | ThrValSerSerAlaSerThrLysGlyProSerValPheProLeuAlaProSerSerLys | 399 |
| Qy | 1196 | AGCACCTCTGGGGGCACAGCGGCCCTGGGCTGCCTGGTCAAGGACTACTTCCCCGAACCG | 1255 |
| Db | 400 | SerThrSerGlyGlyThrAlaAlaLeuGlyCysLeuValLysAspTyrPheProGluPro | 419 |
| Qy | 1256 | GTGACGGTGTCGTGGAACCTCAGGCGCCCTGACCAGCGGCGTGACACCTTCCGGCTGTC | 1315 |
| Db | 420 | ValThrValSerTrpAsnSerGlyAlaLeuThrSerGlyValHisThrPheProAlaVal | 439 |
| Qy | 1316 | CTACAGTCCTCAGGACTCTACTCCCTCAGCAGCGTGGTGACCGTGCCCTCCAGCAGCTTG | 1375 |
| Db | 440 | LeuGlnSerSerGlyLeuTyrSerLeuSerSerValValThrValProSerSerSerLeu | 459 |
| Qy | 1376 | GGCACCCAGACCTACATCTGCAACGTGAAT | 1405 |
| Db | 460 | GlyThrGlnThrTyrIleCysAsnValAsn | 469 |

us-10-698-041-1.rng

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2005, 03:39:44 ; Search time 814 Seconds
(without alignments)
10217.735 Million cell updates/sec

Title: US-10-698-041-1
Perfect score: 1405
Sequence: 1 aaaatgcctggctggtttcg.....cctacatctgcaacgtgaat 1405

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001as:*
- 5: geneseqn2001bs:*
- 6: geneseqn2002as:*
- 7: geneseqn2002bs:*
- 8: geneseqn2003as:*
- 9: geneseqn2003bs:*
- 10: geneseqn2003cs:*
- 11: geneseqn2003ds:*
- 12: geneseqn2004as:*
- 13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|------------|--------|---------------|--------|----|----------|--------------------|
| 1 | 1405 | 100.0 | 1405 | 13 | ADR16814 | Adr16814 Human bre |
| 2 | 1014.8 | 72.2 | 1522 | 8 | ACC00496 | Acc00496 Humanised |
| 3 | 1003 | 71.4 | 1514 | 12 | ADG64751 | Adg64751 Humanised |
| 4 | 985.8 | 70.2 | 1424 | 13 | ADR16815 | Adr16815 Human bre |
| 5 | 958.4 | 68.2 | 5924 | 3 | AAZ38921 | Aaz38921 hCAT1 bin |
| 6 | 958.4 | 68.2 | 5925 | 3 | AAZ38770 | Aaz38770 hCAT1 clo |
| 7 | 937.8 | 66.7 | 2186 | 10 | ADD26469 | Add26469 Phagemid |
| 8 | 937.8 | 66.7 | 2790 | 10 | ADD26467 | Add26467 Phagemid |
| 9 | 937.8 | 66.7 | 2810 | 10 | ADD26471 | Add26471 Phagemid |
| 10 | 936.4 | 66.6 | 1440 | 10 | ADD26475 | Add26475 Phagemid |

| | | | | | us-10-698-041-1.rng | |
|----|-------|------|-------|----|---------------------|--------------------|
| 11 | 923 | 65.7 | 1539 | 8 | AAD56202 | Aad56202 X5 antibo |
| 12 | 916.6 | 65.2 | 1539 | 8 | AAD56203 | Aad56203 X5 antibo |
| 13 | 906.2 | 64.5 | 1680 | 12 | ADF83552 | Adf83552 Anti-tete |
| 14 | 901.4 | 64.2 | 4691 | 2 | AAQ92546 | Aaq92546 pComb3 ex |
| 15 | 901.4 | 64.2 | 6166 | 2 | AAQ92547 | Aaq92547 Expressio |
| 16 | 884.8 | 63.0 | 10251 | 10 | ABZ37478 | Abz37478 CJRA05 nu |
| 17 | 856 | 60.9 | 1526 | 12 | ADN97514 | Adn97514 Artificia |
| 18 | 851.8 | 60.6 | 1551 | 12 | ADN97496 | Adn97496 Artificia |
| 19 | 834.8 | 59.4 | 1566 | 12 | ADN97494 | Adn97494 Artificia |
| 20 | 834 | 59.4 | 2154 | 12 | ADN97490 | Adn97490 Artificia |
| 21 | 820.8 | 58.4 | 1572 | 12 | ADN97492 | Adn97492 Artificia |
| 22 | 820 | 58.4 | 2160 | 12 | ADN97488 | Adn97488 Artificia |
| 23 | 796.8 | 56.7 | 5679 | 13 | ADP79576 | Adp79576 Plasmid p |
| 24 | 779.8 | 55.5 | 6563 | 2 | AAV44953 | Aav44953 Anti-IL-8 |
| 25 | 779.8 | 55.5 | 6563 | 2 | AAX90579 | Aax90579 p6G4V11N3 |
| 26 | 779.8 | 55.5 | 6563 | 3 | AAZ87970 | Aaz87970 Nucleotid |
| 27 | 779.8 | 55.5 | 6563 | 3 | AAC65509 | Aac65509 Anti-IL-8 |
| 28 | 779.8 | 55.5 | 6563 | 8 | ABX63890 | Abx63890 Expressio |
| 29 | 779.8 | 55.5 | 6563 | 8 | ABX81417 | Abx81417 Vector p6 |
| 30 | 779.8 | 55.5 | 6563 | 10 | AAD59311 | Aad59311 p6G4V11 N |
| 31 | 767.8 | 54.6 | 6400 | 3 | AAA53389 | Aaa53389 Expressio |
| 32 | 751.8 | 53.5 | 2000 | 9 | ACC70052 | Acc70052 Nucleotid |
| 33 | 747.4 | 53.2 | 2178 | 2 | AAQ25592 | Aaq25592 Encodes 4 |
| 34 | 747.4 | 53.2 | 2178 | 2 | AAV81689 | Aav81689 4D5 Fab m |
| 35 | 739.6 | 52.6 | 6072 | 2 | AAV63493 | Aav63493 Fab-displ |
| 36 | 739.6 | 52.6 | 6072 | 6 | ABN85200 | Abn85200 Phage-dis |
| 37 | 738.6 | 52.6 | 2143 | 2 | AAX03840 | Aax03840 Plasmid p |
| 38 | 738.6 | 52.6 | 2143 | 5 | AAF31463 | Aaf31463 ps 1130 e |
| 39 | 737.4 | 52.5 | 2050 | 13 | ADR47463 | Adr47463 pTTOD(gH3 |
| 40 | 735.2 | 52.3 | 6072 | 2 | AAV71266 | Aav71266 VEGF huma |
| 41 | 734.6 | 52.3 | 6127 | 2 | AAX07474 | Aax07474 Mus muscu |
| 42 | 734.6 | 52.3 | 6127 | 4 | AAF69253 | Aaf69253 Expressio |
| 43 | 734.6 | 52.3 | 6127 | 12 | ADN07022 | Adn07022 F(ab)-pha |
| 44 | 733.2 | 52.2 | 1951 | 6 | ABQ73919 | Abq73919 Plasmid p |
| 45 | 732.8 | 52.2 | 1477 | 12 | ADQ07674 | Adq07674 Nucleotid |

RESULT 2

ACC00496

ID ACC00496 standard; DNA; 1522 BP.

XX

AC ACC00496;

XX

DT 10-JUL-2003 (first entry)

XX

DE Humanised F3 Fab insert coding sequence.

XX

KW Cytostatic; Platelet-Derived Growth Factor; PDGF; antibody; tumour;

KW cancer; F3 antibody; gene; ds.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT CDS

29..682

FT

/*tag= a

FT

/product= "FAB protein #1"

FT

/transl_except= (pos:98..100,aa:Xaa)

FT

/transl_except= (pos:110..112,aa:Xaa)

FT

/transl_except= (pos:119..121,aa:Xaa)

FT

/transl_except= (pos:155..157,aa:Xaa)

FT

/transl_except= (pos:215..217,aa:Xaa)

FT

/transl_except= (pos:239..241,aa:Xaa)